



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 1635013

TO: Sean McGarry
Art Unit: 1635
Location: rem/2d19/2c18
Serial Number: 097927046

Tuesday, May 17, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

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From: McGarry, Sean
 Sent: Tuesday, May 10, 2005 10:18 AM
 To: STIC-Biotech/ChemLib
 Subject: 73484 SEQ SEARCH 09/927046

Sean McGarry
 AU 1635
 REM 02D19 Office
 REM 2C18 Mailbox
 X20761

Please a search of SEQ ID NOS: 143 and 2332 length limited (nt ≤ 100).

Thank You

seq 143 - 17 NA
 2332 - 38 NA

 STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-
 Date Searcher Picked up: _____
 Date Completed: _____
 Searcher Prep/Rev. Time: _____
 Online Time: _____

 Type of Search

NA #: _____ AA #: _____
 Interference: _____ SPD: _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable

STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
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 Other(Specify): _____

Date completed:

Searcher: Beverly e 2528

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Search Site

____ STIC
 ____ CM-1
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Type of Search

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Vendors

IG
 STN
 Dialog
 APS
 Geninfo
 SDC
 DARC/Questel
 Other CEN

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McGarry, S.
09/927046

09/927046

FILE 'REGISTRY' ENTERED AT 16:17:32 ON 16 MAY 2005
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L2 4 S L1 AND SQL=<100

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L2 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN
RN 495575-86-5 REGISTRY
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HITS AT: 1-17

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OTHER NAMES:
CN 332: PN: WO0211674 SEQID: 2332 claimed RNA
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SEQ 1 ccugcaaucu gaugaggccg uuaggccaa aaaucagg
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HITS AT: 1-38

REFERENCE 1: 136:194272

L2 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN
RN 398240-93-2 REGISTRY
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REFERENCE 1: 136:194272

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L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 15 Feb 2002
ACCESSION NUMBER: 2002:122738 CAPLUS

Searcher : Shears 571-272-2528

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DOCUMENT NUMBER: 136:194272
 TITLE: Ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1
 INVENTOR(S): Thompson, James; McSwiggen, James; McKenzie, Timothy; Ayers, David; Szymkowski, David E.; Grupe, Andrew
 PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA;
 Syntex (U.S.A.) LLC
 SOURCE: PCT Int. Appl., 152 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002011674	A2	20020214	WO 2001-US24970	20010809
WO 2002011674	A3	20030925		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GO, GW, ML, MR, NE, SN, TD, TG				
US 2003064946	A1	20030403	US 2001-927046	20010809
PRIORITY APPLN. INFO.:			US 2000-224383P	P 20000809

AB Nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNAzymes, and GeneBlocs, which modulate the expression of calcium-activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4) are provided. A target discovery target validation approach was used for finding genes that are involved in chronic mucous hypersecretion. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for green fluorescent protein (GFP). The promoter region of the GFP gene is replaced by a portion of the mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene; the plasmid also contains the neomycin drug resistance gene. The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. A ribozyme library with two randomized regions comprising six-nucleotide binding "arms" is used to enrich cells for non-responders to mucin induction and a bioinformatics approach used to identify human CLCA1 as a regulator of MUC5AC expression. Antisense, hammerhead, DNAzyme, NCH, amberzyme, zinzyme, and G-Cleaver ribosome binding/cleavage sites in CLCA1 were identified. The nucleic acid mols. are individually analyzed by computer folding to assess whether the sequences fold into the appropriate secondary structure and to anneal to various sites in the RNA target. Those nucleic acid mols. with unfavorable intramol. interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

IT 398240-93-2

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09/927046

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(CLCA-1 gene target region for hammerhead ribozyme; ribozymes and
antisense oligonucleotides for the inhibition of gene expression by
calcium-activated chloride channel-1 gene CLCA-1)

IT 399091-50-0

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study);
USES (Uses)
(hammerhead ribozyme; ribozymes and antisense oligonucleotides for
the inhibition of gene expression by calcium-activated chloride
channel-1 gene CLCA-1)

(FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:21:55 ON 16 MAY 2005)

L4 O S L2

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09/927046

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DEL HIS Y

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L4 0 S L2

FILE 'HOME' ENTERED AT 16:22:05 ON 16 MAY 2005

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KC Garry, S.
091927046 Page 1
Seg. 1D 14322332

OM nucleic - nucleic search, using bw model
Run on: May 13, 2005, 16:49:04 ; Search time 488.055 Seconds
Copyright (c) 1993 - 2005 Compugen Ltd.

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Total number of hits satisfying chosen parameters:	1 IDENTITY_NUC Gapop 10.0 , Gapext 1.0				
Minimum DB seq length:	4708233 seqs, 24227607955 residues				
Maximum DB seq length:	0				
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Maximum Match 100%					
Listing first 100 summaries					
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14:	gb_vl:*				
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SUMMARIES					
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1	17	100.0	17	6 AX578305	AX578305 Sequence
2	16	94.1	17	6 AX578304	AX578304 Sequence
3	16	94.1	17	6 AX578867	AX578867 Sequence
4	15	88.2	15	6 AX583575	AX583575 Sequence
5	15	88.2	15	6 AX583576	AX583576 Sequence
6	15	88.2	15	6 AX583577	AX583577 Sequence
7	15	88.2	17	6 AX578303	AX578303 Sequence
8	15	88.2	88	6 CQ306794	CQ306794 Sequence
9	14	82.4	15	6 AX583574	AX583574 Sequence
10	14	82.4	17	6 AX578306	AX578306 Sequence
11	14	82.4	19	6 AX692118	AX692118 Sequence
12	13	78.8	22	6 AX771264	AX771264 Sequence
13	13	78.8	52	6 AX556812	AX556812 Sequence
14	13	76.5	15	6 AX583578	AX583578 Sequence
15	13	76.5	17	6 AX579409	AX579409 Sequence
16	13	76.5	17	6 AX579833	AX579833 Sequence
17	13	76.5	60	6 CQ549043	CQ549043 Sequence
18	13	76.5	67	6 AX498484	AX498484 Sequence
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REFERENCE AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)

JOURNAL Patent: WO 0211674-A 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES source

ORIGIN

Query Match Best Local Similarity 64.7%; Pred. No. 2.6e+02; Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

/mol_type="unassigned RNA"
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REFERENCE AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)

JOURNAL Patent: WO 0211674-A 705 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES source

ORIGIN

Query Match Best Local Similarity 62.5%; Pred. No. 9.4e+02; Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)

JOURNAL Patent: WO 0211674-A 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES source

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ACCESSION	AX583574	AX583574						
VERSION	AX583574.1	GI:27655384						
KEYWORDS	.							
SOURCE	synthetic construct							
ORGANISM	synthetic construct							
REFERENCE	other sequences; artificial sequences.							
AUTHORS	Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowiak,D.E.							
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)							
JOURNAL	Patent: WO 0211674-A 5412 14-FEB-2002;							
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)								
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DEFINITION	Sequence 144 from Patent WO0211674.							
ACCESSION	AX578306	AX578306						
VERSION	AX578306.1	GI:27647508						
KEYWORDS	.							
ORGANISM	Homo sapiens (human)							
REFERENCE	Bukaricota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo.							
AUTHORS	Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowiak,D.E.							
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)							
JOURNAL	Patent: WO 0211674-A 144 14-FEB-2002;							
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)								
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DEFINITION	Sequence 17 from Patent EP1367120.							
ACCESSION	AX56812	AX56812.1	GI:40785287					
VERSION								
KEYWORDS	.							

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	Takeshima,S., Sogabe,A. and Oka,M.
TITLE	Modified pyrroloquinoline quinone (POQ) dependent glucose dehydrogenase with superior substrate specificity and stability
JOURNAL	Patent: EP 1367120-A 17-03-DEC-2003;
FEATURES	TOYO BOSEKI KABUSHIKI KAISHA (JP)
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ORGANISM	
REFERENCE	1. Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grupe,A.
AUTHORS	Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
TITLE	Patent: WO 0211674-A 5416 14-FEB-2002;
JOURNAL	RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
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ACCESSION	AX579409
VERSION	AX579409
KEYWORDS	
ORGANISM	Homo sapiens (human)
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
Source	
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ORIGIN	
Query Match	76.5%; Score 13; DB 6; Length 17;
Best Local Similarity	53.8%; Pred. No. 4.7e+04;
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ACCESSION	C0549043
VERSION	C0549043.1
KEYWORDS	
ORGANISM	Homo sapiens (human)
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
Source	
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Best Local Similarity	53.8%; Pred. No. 4.7e+04;
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ACCESSION	C0549043
VERSION	C0549043
KEYWORDS	
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REFERENCE	
AUTHORS	Shoshan,A., Wasserman,A., Mintz,B., Mintz,L. and Paigler,S.
TITLE	Oligonucleotide library for detecting rna transcripts and splice

variants that populate a transcriptome
JOURNAL WO 021049-A 18678 07-FEB-2002;
FEATURES Compugen Inc. (US) Location/Qualifiers
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Gaps 0;

Qy 4 GAUUCAUUGCG 16
Db 30 GATTCAATGCG 42

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LOCUS Sequence 18 from Patent WO20059371.
DEFINITION 67 bp DNA linear PAT 26-SEP-2002
ACCESSION AX496844
VERSION AX496844.1 GI:23342364
KEYWORDS synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 25468 09-AUG-2001;
Genome-wide location and function of dna binding proteins
Patent: WO 0205371-A 18 01-AUG-2002;
WHITEHEAD BIOMEDICAL INST (US)
FEATURES Location/Qualifiers
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Db 43 TGAATTCAAGCA 31

RESULT 19

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LOCUS C0081942 Sequence 17742 from Patent WO0157278.
DEFINITION 80 bp DNA linear PAT 20-JAN-2004
ACCESSION CQ081942
VERSION CQ081942.1 GI:41051811
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelial cells
Patent: WO 0157278-A 17742 09-AUG-2001;
Acomica, Inc. (US)
FEATURES Location/Qualifiers
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ORIGIN

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Matches 9; Conservative 5; Mismatches 2; Indels 0;
Gaps 0;

Qy 2 CUGAUCUCAUGCAG 17
Db 57 CTGATTCATTCAGG 42

RESULT 20

CQ116609/C
LOCUS Sequence 25468 from Patent WO0157272.
DEFINITION 80 bp DNA linear PAT 21-JAN-2004
ACCESSION CQ116609
VERSION CQ116609.1 GI:41086479
KEYWORDS Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 25468 09-AUG-2001;
Genome-wide location and function of dna binding proteins
Patent: WO 0205371-A 18 01-AUG-2002;
WHITEHEAD BIOMEDICAL INST (US)
FEATURES Location/Qualifiers
source 1. .80
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AB002059.1, EVALUE 6.00e-38"
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AB002059.1, EVALUE 6.00e-38"

ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 80;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0;
Gaps 0;

Qy 2 CUGAUCUCAUGCAG 17
Db 57 CTGATTCATTCAGG 42

RESULT 21

CQ155325/C
LOCUS C0155325 Sequence 25347 from Patent WO0157276.
DEFINITION 80 bp DNA linear PAT 21-JAN-2004
ACCESSION CQ155325
VERSION CQ155325.1 GI:41162677
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 015276-A 25347 09-AUG-2001;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"

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Qy 2 CUGAATUCAUGCAGG 17	VERSION			
Db 57 CTGATGCAATTTCAGG 42	KEYWORDS			
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ACCESSION	80 bp DNA	LOCUS		
VERSION	80 bp DNA	DEFINITION		
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SOURCE		VERSION		
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AUTHORS				

FEATURES		AUTHORS
Source		Clarke, J.H.
	Location/Qualifiers	1. .80
	/organism="Homo sapiens"	/DEFINITION Direct Submission
	/mol_type="unassigned DNA"	JOURNAL Submitted (22-MAR-2004) Clarke, J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK
	/db_xref="taxon:9606"	COMMENT AR denotes an activation tag dissociation transposon within a single line; ER an enhancer trap dissociation transposon; MT a mis-expression suppressor mutator transposon. SM a defective suppression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon. _5 denotes a sequence derived from the 5' end of the transposon. BBSRC GARRET, ATIS project On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock code: N17484.
Qy	Query Match Similarity 75.3%; Score 12.8; DB 6; Length 80; Best Local Similarity 56.2%; Pred. No. 5.7e+04; Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	RESULT 26
Db	: :: : : CTGATTCATTCAGG 42	CQ350689/C
		LOCUS C0350689 Sequence 24783 from Patent WO0157275.
		DEFINITION 80 bp DNA
		ACCESSION C0350689
		VERSION C0350689.1 GI:41299760
		KEYWORDS Homo sapiens (human)
		SOURCE Homo sapiens
		ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	I. Penn, S.G., Hanezel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain	Aeomica, Inc. (US)
AUTHORS		JOURNAL Patent: WO 0157275-A 24783 09-AUG-2001;
TITLE		FEATURES
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SOURCE	/organism="Homo sapiens"	1. .86
	/mol_type="unassigned DNA"	/organism="Arabidopsis thaliana"
	/db_xref="taxon:9606"	/variety="Landsberg erecta NASC stock code NW20"
	/note="MAP TO AC02472 3-EXPRESSED IN BRAIN SIGNAL = 13-EST HUMAN HIT: BF31.025.1, EVALUE 1.00e-37-NT HIT: AB02059.1, EVALUE 6.00e-38"	/clone="AP001305"
		/standard_name="GT_3_7348"
ORIGIN		RESULT 28
Query Match Similarity 75.3%; Score 12.8; DB 6; Length 80; Best Local Similarity 56.2%; Pred. No. 5.7e+04; Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	LOCUS C0001210 Sequence 12672 from Patent EP1260592.	
DEFINITION 100 bp DNA	DEFINITION	
ACCESSION C0001210	ACCESSION	
VERSION C0001210.1 GI:41007848	VERSION	
KEYWORDS	SOURCE	
	Bacillus cereus	
	ORGANISM	
	Bacillus cereus; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
REFERENCE	1	REFERENCE
AUTHORS	Donner, H., Drescher, B., Huber, A. and Weber, J.	AUTHORS
TITLE	Biochip	TITLE
JOURNAL	Patent: EP 1260592-A 12672 27-NOV-2002; MWG -Biotech AG (DE)	JOURNAL
FEATURES	LOCATION/QUALIFIERS	FEATURES
SOURCE	1. .100	LOCATION/QUALIFIERS
	/organism="Escherichia coli"	1. .100
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	/note="Yi41.b4279 U00096 complement(4499671_4500999)"	/note="Yi41.b4279 U00096 complement(4499671_4500999)"
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CR378747/c	Query Match Similarity 75.3%; Score 12.8; DB 6; Length 100; Best Local Similarity 62.5%; Pred. No. 5.7e+04; Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	LOCUS AX998611 Sequence 10074 from Patent EP1260592.
LOCUS CR378747	DEFINITION 100 bp DNA	DEFINITION
DEFINITION Arabidopsis thaliana transposon insertion STS GT_3_7348, sequence tagged site.	ACCESSION AX998611	ACCESSION AX998611
ACCESSION CR378747	VERSION	VERSION
VERSION CR378747.1 GI:45725203	KEYWORDS	
STS; STS, sequence tagged site.	SOURCE	
ORGANISM Arabidopsis thaliana (thale cress)	ORGANISM	
Bukavuva; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Eudicots; Core eudicots; Rosids; Eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE 1 Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., Legrys, C., Jones, J.D.G. and Bevan, M.		
AUTHORS JOURNAL Unpublished		
REFERENCE 2 (bases 1 to 86)		

KEYWORDS Escherichia coli
ORGANISM Escherichia coli
REFERENCE Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1. Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE Blochig
JOURNAL Patent: EP 1260592-A 10074 27-NOV-2002;
MWG - Biotech AG (DE)
FEATURES Location/Qualifiers
Source 1. .100
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="inta b2623 U00096 2754180_2755421"
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Query Match Best Local Similarity 75.3%; Score 12.8; DB 6; Length 100;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGUGAUUCAUUCCAG 16
Db 82 CCTGGATGTCATTTGAAG 97

RESULT 30 AR298188/C AR298188 DEFINITION Sequence 9923 from patent US 6537751.
ACCESSION AR298188
VERSION AR298188.1
KEYWORDS Unknown.
SOURCE Unclassified.

REFERENCE Cohen,D., Chumakov,I. and Blumenfeld,M.
AUTHORS Title Bi allelic markers for use in constructing a high density
SEQUENCE disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9923 25-MAR-2003;
FEATURES Source Location/Qualifiers
1. .20 /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match Best Local Similarity 50.0%; Score 12.4; DB 6; Length 20;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUCCAG 14
Db 20 CCTGGATGTCATTTGAAG 7

RESULT 31 C0759952/C C0759952 DEFINITION Sequence 2 from Patent EP1382685.
ACCESSION C0759952
VERSION C0759952.1
KEYWORDS Synthetic construct
ORGANISM Other sequences; artificial sequences.

REFERENCE Kleijng, M. and Siebelt, N.
AUTHORS Title Process for the fermentative preparation of L-amino acids using
strains of the enterobacteriaceae family with overexpressed rseB
gene
JOURNAL Patent: EP 1382685-A 2 21-JAN-2004;

FEATURES Source
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

FEATURES source Degussa AG (DE)
ORGANISM Degussa AG (DE)
REFERENCE 1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:33630"
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Query Match Best Local Similarity 72.9%; Score 12.4; DB 6; Length 25;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUUCAUUCCAG 16
Db 21 TGATTTCAGTCGAG 8

RESULT 32 AX683923/C AX683923 DEFINITION Sequence 4 from Patent WO03008612.
ACCESSION AX683923
VERSION AX683923.1
KEYWORDS SOURCE synthetic construct
ORGANISM OTHER SEQUENCES; ARTIFICIAL SEQUENCES.

REFERENCE Rieping, M.
AUTHORS Title Process for the preparation of L-amino acids using strains of the
Enterobacteriaceae family which contain an enhanced rseA or rsec
Gene
JOURNAL Patent: WO 03008612-A 4 30-JAN-2003;
Degussa AG (DE)
FEATURES Source Location/Qualifiers
1. .25 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:33630"
/note="Primer rsecC2"

ORIGIN

Query Match Best Local Similarity 57.1%; Score 12.4; DB 6; Length 25;
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Qy 3 UGAUUCAUUCCAG 16
Db 21 TGATTTCAGTCGAG 8

RESULT 33 C0794144/C C0794144 DEFINITION Sequence 64 from Patent EP1403384.
ACCESSION C0794144
VERSION C0794144.1
KEYWORDS SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Meijer, C.J. and Snijders, P.J.
TITLE Method for detecting and typing of cutaneous HPV and primers and
probes for use therein
JOURNAL Patent: EP 1403384-A 64 31-MAR-2004;
Stichting Researchfonds Pathologie (NL)
FEATURES Source
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

misc_feature 1. . .30
/note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
 Best Local Similarity 57.1%; Pred. No. 1e+05; DB 6; Length 30;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGAUAUCAUGC 14
 Db 14 CCTGAGTCATGCC 1

RESULT 34
CQ794148/c
LOCUS CQ794148 Sequence 68 from Patent EP1403384.
DEFINITION 30 bp DNA linear PAT 19-APR-2004
ACCESSION CQ794148
VERSION CQ794148.1 GI:46406790
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

1 Meijer, C.J. and Snijders, P.J.
 Method for detecting and typing of cutaneous HPV and primers and
 probes for use therein
 Patent: EP 1403384-A 68 31-MAR-2004;
 Stichting Researchfonds Pathologie (NL)

FEATURES
source

1. .30
 /organism="Human papillomavirus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10566"
 1. .30
 /note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
 Best Local Similarity 57.1%; Pred. No. 1e+05; DB 6; Length 30;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGAUAUCAUGC 14
 Db 14 CCTGAGTCATGCC 1

RESULT 35
CQ800113/c
LOCUS CQ800113 Sequence 64 from Patent WO2004029302.
DEFINITION 30 bp DNA linear PAT 29-APR-2004
ACCESSION CQ800113
VERSION CQ800113.1 GI:46849034
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE
 1 Meijer, C.J. and Snijders, P.J.
 Method for detecting and typing of cutaneous hpv and primers and
 probes for use therein
 Patent: WO 2004029302-A 64 08-APR-2004;
 Stichting Researchfonds Pathologie (NL)

FEATURES
source

1. .30
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 /mol_type="unassigned DNA"
 /db_xref="taxon:10566"
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 /note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
 Best Local Similarity 57.1%; Pred. No. 1e+05; DB 6; Length 30;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGAUAUCAUGC 14
 Db 14 CCTGAGTCATGCC 1

RESULT 36
CQ800117/c
LOCUS CQ800117 Sequence 68 from Patent WO2004029302.
DEFINITION 30 bp DNA linear PAT 29-APR-2004
ACCESSION CQ800117
VERSION CQ800117.1 GI:46849038
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

1 Meijer, C.J. and Snijders, P.J.
 Method for detecting and typing of cutaneous hpv and primers and
 probes for use therein
 Patent: WO 2004029302-A 68 08-APR-2004;
 Stichting Researchfonds Pathologie (NL)

FEATURES
source

1. .30
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 /mol_type="unassigned DNA"
 /db_xref="taxon:10566"
 1. .30
 /note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
 Best Local Similarity 57.1%; Pred. No. 1e+05; DB 6; Length 30;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGAUAUCAUGC 14
 Db 14 CCTGAGTCATGCC 1

RESULT 37
AR171877/c
LOCUS AR171877 Sequence 10 from patent US 6297365.
DEFINITION 49 bp DNA linear PAT 17-DEC-2001
ACCESSION AR171877
VERSION AR171877.1 GI:17910827
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
 1 (base 1 to 49)
AUTHORS Adams, C.C., Brentano, S.T. and Schroth, G.P.
TITLE Decoy probes
JOURNAL Patent: US 6297365-A 10 02-OCT-2001;
FEATURES
source

1. .49
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 /mol_type="unassigned DNA"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 49;
 Best Local Similarity 57.1%; Pred. No. 9.8e+04; DB 6; Length 49;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

FEATURES
source

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Db	25 tgatttcagtcgcag 12	RESULT 40 BD222952/c	RESULT 38 AR171878/c
Qy	3 ugauucauugcag 16 ; :: : : 12	LOCUS BD222952/c	LOCUS AR171878
Db	25 tgatttcagtcgcag 12	DEFINITION Reversible inhibitory probe.	DEFINITION Sequence 11 from patent US 6297365.
Qy	3 ugauucauugcag 16 ; :: : : 12	ACCESSION BD222952	ACCESSION AR171878
Db	25 tgatttcagtcgcag 12	VERSION JP 200521070-A/11	VERSION AR171878.1 GI:17910828
Qy	3 ugauucauugcag 16 ; :: : : 12	KEYWORDS synthetic construct	KEYWORDS Unknown.
Db	25 tgatttcagtcgcag 12	SOURCE ORGANISM Unknown. Unclassified.	SOURCE ORGANISM
Qy	3 ugauucauugcag 16 ; :: : : 12	REFERENCE 1. (bases 1 to 49) ADAMS, C.C., BRENTANO, S.T. and SCHROTH, G.P.	REFERENCE 1. (bases 1 to 49)
Db	25 tgatttcagtcgcag 12	AUTHORS ADAMS, C.C., BRENTANO, S.T. and SCHROTH, G.P.	AUTHORS ADAMS, C.C., BRENTANO, S.T. and SCHROTH, G.P.
Qy	3 ugauucauugcag 16 ; :: : : 12	TITLE Decoy probes	TITLE Decoy probes
Db	25 tgatttcagtcgcag 12	JOURNAL Patent: US 6297365-A 11 02-OCT-2001; Location/Qualifiers	JOURNAL Patent: JP 200521070-A 11 16-JUL-2002;
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Db	25 tgatttcagtcgcag 12	ORIGIN	ORIGIN
Qy	3 ugauucauugcag 16 ; :: : : 12	Query Match Best Local Similarity 57.1%; Pred. No. 9.8e+04; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	Query Match Best Local Similarity 72.9%; Score 12.4; DB 6; Length 49; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db	25 tgatttcagtcgcag 12	COMMENT OS Synthetic construct PN Jp 200521070-A/10 PD 16-JUL-2002 PP 30-JUL-1993 JP 200562561 PR 31-JUL-1998 US 60/054979 PI CHRISTOPHER C ADAMS, STEVEN T BRENTANO, GARY P SCHROTH PC CL2N15/09, CL2O1/68, G01N33/50, CL2W15/00 CC Reversible inhibitory probe FH Key FT source FT location/Qualifiers	COMMENT OS Synthetic construct PN Jp 200521070-A/11 PD 16-JUL-2002 PP 30-JUL-1999 JP 2000562561 PR 31-JUL-1998 US 60/054979 PI CHRISTOPHER C ADAMS, STEVEN T BRENTANO, GARY P SCHROTH PC CL2N15/09, CL2O1/68, G01N33/50, CL2W15/00 CC Reversible inhibitory probe FH Key FT source FT location/Qualifiers
Qy	3 ugauucauugcag 16 ; :: : : 12	FEATURES source /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	FEATURES source /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
Db	25 tgatttcagtcgcag 12	ORIGIN	ORIGIN
Qy	3 ugauucauugcag 16 ; :: : : 12	Query Match Best Local Similarity 57.1%; Pred. No. 9.8e+04; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	Query Match Best Local Similarity 72.9%; Score 12.4; DB 6; Length 49; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db	25 tgatttcagtcgcag 12	SEARCH COMPLETED: MAY 13, 2005, 18:17:10 JOB TIME : 497.055 SEC_B	SEARCH COMPLETED: MAY 13, 2005, 18:17:10 JOB TIME : 497.055 SEC_B
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Qy	3 ugauucauugcag 16 ; :: : : 12	ORIGIN	ORIGIN
Db	25 tgatttcagtcgcag 12	Query Match Best Local Similarity 57.1%; Pred. No. 9.8e+04; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	Query Match Best Local Similarity 72.9%; Score 12.4; DB 6; Length 49; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:40:53 ; Search time 123.327 Seconds
 (without alignments)
 816.004 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccugauuucauugcagg 17

Scoring table: IDENTITY_NUC

Searched: Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	100.0	17	6 ABR55772	Abk55772 Human CIC
2	16	94.1	17	6 ABR56334	Abk56334 Human CIC
3	16	94.1	17	6 ABR55771	Abk55771 Human CIC
4	15	88.2	15	6 ABR61042	Abk61042 Human CIC
5	15	88.2	15	6 ABR61044	Abk61044 Human CIC
6	15	88.2	15	6 ABR61043	Abk61043 Human CIC
7	15	88.2	17	6 ABR55770	Abk55770 Human CIC
8	15	88.2	88	6 ABS17908	Abs17908 Human gen
9	14	82.4	15	6 ABK61041	Abk61041 Human CIC
10	14	82.4	17	6 ABK55773	Abk55773 Human CIC
11	14	82.4	19	10 ADG70258	ADG70258 CILDB exp
c	12	78.8	22	9 ACCT0300	ACCT0300 PCR prime
c	13	78.8	52	12 ADG16067	Adg16067 PQGDH mu
c	14	78.8	66	2 AAT20442	Aat20442 Human gen
c	15	76.5	15	6 ABK61045	Abk61045 Human CIC
c	16	76.5	17	6 ABK56876	Abk56876 Human CIC
c	17	76.5	17	6 ABK57300	Abk57300 Human CIC
c	18	76.5	43	12 ADP7171	Adp7171 C. albica
c	19	76.5	60	6 ABR45930	Abn45930 Human sp1
20	12.8	75.3	20	2 AAV51603	AAv51603 Zea maya

Ack08857 Human mic
 Abk33718 S. pneumo
 Aav50992 Maize pol
 Aav50971 Maize pol
 Aav50981 Maize pol
 Aav50994 Maize pol
 Aav47798 Maize pol
 Aav47809 Maize pol
 Aav47788 Maize pol
 Aah86424 Human bin
 Aai27809 Probe #17
 Abt76122 Human toe
 Aai56782 Probe #25
 Abt40577 Probe #19
 Aak50790 Human bon
 Aak4792 Human bra
 Abs50382 Human liv
 Abt24274 Human gen
 Acd81396 E. coli K
 Acd78798 E. coli K
 Adt70081 Human GIP
 Adt69966 Human GIP
 Aazz5567 Human bia
 Aal52075 Escherich
 Adt45223 Enterobac
 Adr37819 Rettinobla
 Aav47787 Maize pol
 Aav47796 Maize pol
 Aav47811 Maize pol
 Aav47785 Maize pol
 Aav47795 Maize pol
 Aaz269384 Human map
 Aazz5332 Decay pro
 Aaz50531 Decay pro
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 Adt101975 ATFaipha
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 Adt00946 Human VEG
 Adt0085 Human VEG
 Adt00820 Human VEG
 Abt13166 Fanconi a
 Adc42403 Human FAN
 Adt00821 Human VEG
 Abk15883 Serrate 1
 Aax79100 Human c-R
 Aazz91969 Mahogany
 Abt55052 Human G-P
 Aaa25050 Primer Fo
 Abq84189 P structu
 Abq49706 Human kin
 Aah96752 Human Chk
 Abk48079 Human zin
 Abk48080 Human zin
 Abk60945 Tight jun
 Abk60946 Tight jun
 Adm33116 Rat granz
 Adm3117 Rat granz
 Adm0357 K. lactis
 Adh08358 K. lactis
 Aai17518 Human sil
 Abn33559 Human spl
 Abn44704 Human spl
 Abn3629 Human spl
 Abn58185 Mouse spl
 Abn51685 Mouse spl
 Ads60391 Corn seed
 Acd7938 E. coli K
 Acd74179 E. coli K

QY	2	CUGAUUCAUNGAGG	17	Db	2	CCUGATUTCATUGCAG	17
Db	1	CUGAUUCAUNGAGG	16	RESULT 3			
ID	ABK5571	ABK5571 standard; RNA; 17 BP.		RESULT 4			
ID	ABK61042	ABK61042 standard; DNA; 15 BP.		AC	AC		
AC	ABK5571;			AC	ABK61042;		
AC	XX			XX	XX		
DT	02-JUL-2002	(first entry)		DT	02-JUL-2002	(first entry)	
XX				XX			
DB	Human CLCA1 gene enzymatic nucleic acid #142.			XX	Human CLCA1 gene enzymatic nucleic acid #5413.		
XX				XX			
KW	Human; chloride channel calcium activated 1; CLCA1; BS; antiasthmatic; antiinflammatory; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.			XX	Human; chloride channel calcium activated 1; CLCA1; BS; antiasthmatic; antiinflammatory; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.		
KW				XX			
KW	oxygene therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.			OS	Homo sapiens.		
XX				XX			
OS	Homo sapiens.			PN	WO200211674-A2.		
XX				XX			
PN	WO200211674-A2.			PD	14-FEB-2002.		
XX				PP	09-AUG-2001; 2001WO-US024970.		
PD	14-FEB-2002.			XX	09-AUG-2000; 2000US-0224383P.		
XX				PR	(RIBO-) RIBOZYME PHARM INC.		
PP	09-AUG-2001; 2001WO-US024970.			PA	(SYNT) SYNTEX USA LLC.		
XX				PA	(THOM/) THOMPSON J.		
PR	09-AUG-2000; 2000US-0224383P.			PA	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
XX				PI	Grupe A;		
PA	(RIBO-) RIBOZYME PHARM INC.			PT	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
PA	(SYNT) SYNTEX USA LLC.			PT	Grupe A;		
PA	(THOM/) THOMPSON J.			PT	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
XX				DR	DR		
PI	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;			XX	14-FEB-2002.		
PI	Grupe A;			XX	09-AUG-2001; 2001WO-US024970.		
XX				XX	09-AUG-2000; 2000US-0224383P.		
DR	14-FEB-2002.			PR	(RIBO-) RIBOZYME PHARM INC.		
XX				PA	(SYNT) SYNTEX USA LLC.		
XX				PA	(THOM/) THOMPSON J.		
XX				PA	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
XX				PI	Grupe A;		
XX				PT	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
XX				PT	Grupe A;		
XX				PT	Thompson J., Mcaviggen J., McKenzie T., Ayers D., Szymkowski DE;		
XX				PS	WPI; 2002-217145/27.		
XX				XX	WPI; 2002-217145/27.		
PS	Claim 4; Page 55; 152pp; English.			XX	Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.		
PS	Claim 4; Page 55; 152pp; English.			PT	Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.		
XX	The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention			PT	Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention		
XX	Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
SQ	Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Query Match	94.1%; Score 16; DB 6; Length 17;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Best Local Similarity	100.0%; Pred. No. 2.1e+02;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
QY	1 CCGAUUCAUNGAG 16			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Db	1 CCTGATTCATGCA 15			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
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Best Local Similarity	60.0%; Pred. No. 6.7e+02;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Matches	9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
QY	1 CCTGATTCATGCA 15			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		
Db	1 CCTGATTCATGCA 15			XX	Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;		

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 XX
 DT 02-JUL-2002 (first entry)
 DE Human CLCA1 gene enzymatic nucleic acid #5415.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PR 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE,
 PI Grupe A;
 XX
 DR WPI; 2002-217145/27.
 XX
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XX
 PS Claim 4; Page 139; 152pp; English.
 XX
 The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell, or
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 88.2%; Score 15; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 6.7e+02;
 Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 3 UGAUUAUCAUUGCAGG 17
 QY :|::|::|::|::|::|::|::|
 DB 1 TGATTTCATGGAG 15
 RESULT 6
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 ID ABK61043 standard; DNA; 15 BP.
 XX
 AC ABK55770
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 AC ABK55770 standard; RNA; 17 BP.
 XX
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 XX

XK ABK61043;
 AC
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 DT 02-JUL-2002 (first entry)
 DE Human CLCA1 gene enzymatic nucleic acid #5414.
 XK
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XK
 OS Homo sapiens.
 XK
 PN WO200211674-A2.
 XK
 PD 14-FEB-2002.
 XK
 PP 09-AUG-2001; 2001WO-US024970.
 XK
 PR 09-AUG-2000; 2000US-0224383P.
 XK
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE,
 PI Grupe A;
 XK
 DR WPI; 2002-217145/27.
 XK
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XK
 PS Claim 4; Page 139; 152pp; English.
 XK
 The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XK
 Sequence 15 BP; 3 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
 SQ Query Match 88.2%; Score 15; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 6.7e+02;
 Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CUGAUUAUCAUUGCAG 16
 QY :|::|::|::|::|::|
 DB 1 CTGATTTCATGGAG 15
 RESULT 7
 ABK55770
 ID ABK55770 standard; RNA; 17 BP.
 XX
 AC ABK55770;

DT 02-JUL-2002 (first entry)
 XX Human CLCA1 gene enzymatic nucleic acid #141.
 DB Human; chloride channel calcium activated 1; CLCA1; BB; antiasthmatic;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW chronic bronchitis; chronic obstructive pulmonary disease; COPD; asthma;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; muokinetic;
 KW acetylcysteine.
 XX OS Homo sapiens.
 XX PN WO200211674-A2.
 XX PD 14-FEB-2002.
 XX PP 09-AUG-2001; 2001WO-US024970.
 XX PR 09-AUG-2000; 2000US-0224383P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT-) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX DR WPI; 2002-217145/27.
 XX PT Enzymatic polynucleotide that down regulates expression of chloride
 channel calcium activated gene, useful for treating Chronic obstructive
 pulmonary disease (COPD), chronic bronchitis and asthma.
 XX PS Claim 4; Page 55; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down
 regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 by cleaving RNA derived from the genes. The nucleic acid sequences are
 useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 SQ Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 88.2%; Score 15; DB 6; Length 17;
 . Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUCAUAGCA 15
 Db 3 CCUGAUUCAUAGCA 17

RESULT 8
 ABS17908 ABS17908 standard; DNA; 88 BP.
 ID ABS17908
 XX ABS17908;
 AC ABS17908;
 DT 19-AUG-2002 (first entry)
 DB Human genome-derived single exon probe ORF from lung SEQ ID No 17899.

XX Human; dg; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW family idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; Gaucher's disease; Niemann-Pick disease;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PP 30-JAN-2001; 2001WO-US000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2002-114183/15.
 XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 measure gene expression in human lung sample.
 XX PS Claim 4; SEQ ID NO 17899; 634pp; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarray having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probe/open reading frame (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Kartagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the

CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 88 BP; 27 A; 24 C; 12 G; 25 T; 0 U; 0 Other;
 Best Local Similarity 60.0%; Pred. No. 7; 8e+02; 6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 6; Mismatches 0;

Qy 1 ccugauucatcgca 15
 ||:||::||:||:||:
 Db 63 CCTGATTTCATGCA 77

RESULT 9
 ABK61041
 ID ABK61041 standard; DNA; 15 BP.
 XX
 AC ABK61041;
 XX
 DT 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #5412.

XX Human; chloride channel calcium activated 1; CLCA1; ss: antiasthmatic;
 XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 XX acetylcysteine.

XX OS Homo sapiens.

XX PN WO200211674-A2.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PD 14-FEB-2002.

XX PR 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PR 09-AUG-2001; 2001WO-US024970.

XX PR (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT-) SYNTEX USA LLC.
 PA (THOM-) THOMPSON J.

XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX DR WPI; 2002-217145/27.

XX PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 4; Page 138; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention

xX Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
 SQ Sequence 88 BP; 27 A; 24 C; 12 G; 25 T; 0 U; 0 Other;
 Best Local Similarity 82.4%; Score 14; DB 6; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.2e+03; 8; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 6; Mismatches 0;

Qy 1 ccugauucatcgca 14
 ||:||::||:||:
 Db 2 CCTGATTTCATGCA 15

RESULT 10
 ABK55773
 ID ABK55773 standard; RNA; 17 BP.
 XX
 AC ABK55773;
 XX
 DT 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #144.

XX Human; chloride channel calcium activated 1; CLCA1; ss: antiasthmatic;
 XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 XX acetylcysteine.

XX OS Homo sapiens.

XX PN WO200211674-A2.

XX PR 14-FEB-2002.

XX PR 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PR (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT-) SYNTEX USA LLC.
 PA (THOM-) THOMPSON J.

XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX DR WPI; 2002-217145/27.

XX PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 4; Page 55; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention

SQ Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

Oy	4	GAAUCAUGCGG	17	Oy	4	GAAUCAUGCAGG	17
Db	1	GAUUCAUGCGG	14	Db	19	GATTGATTCAGG	6
RESULT 11				RESULT 12			
ID	ADG70258/C			ID	ACC70300		
ID	ADG70258			ID	ACC70300 standard		
AC				DB			
XX				XX			
AC	ADG70258;			AC	ACC70300;		
DT	11-MAR-2004	(first entry)		DT	11-AUG-2003	(first entry)	
XX				XX			
XX				PCR	Primer used to isolate cDNA encoding the human mucinase AMCase.		
DB	CILD8 exon 12 and ANGE exon 3 SNP identification primer #74.			XX			
XX	ANGE; CILD8; CILD7; ANGE-CILD8; ANGE-CILD7; CILD7-CILD8;			KW	Human; mucinase; AMCase; mucin; enzyme; chitin; cystic fibrosis;		
KW	ANGE-CILD8-CILD7; anti-allergic; anti-asthmatic; dermatological;			KW	tuberculosis; mucin-producing tumour; protozoan parasite; primer; ss.		
KW	anti-pyretic; anti-inflammatory; gene therapy; IgB-mediated disease;			OS	Homo sapiens.		
KW	primer; ss.			XX			
XX	Unidentified.			PN	WO2003038079-A2.		
OS				XX			
XX				PD	08-MAY-2003.		
PN	WO2003000727-A2.			XX			
XX				PP	01-NOV-2002; 2002WO-NL000694.		
XX				XX			
PD	03-JAN-2003.			PR	02-NOV-2001; 2001US-0004219.		
XX				XX			
PP	21-JUN-2002; 2002WO-GB002859.			PA	(MACR-) MACROZIME BV.		
XX				XX			
PR	21-JUN-2001; 2001GB-00015211.			PI	Aerts JMEG, Boot RG;		
PR	21-JUN-2001; 2001GB-00015212.			XX			
PR	21-JUN-2001; 2001GB-00015213.			DR	WPI; 2003-457394/43.		
XX				XX			
PA	(ISIS-) ISIS INNOVATIONS LTD.			PT	New recombinant and/or isolated or purified mammalian mucinase or its modified form, useful for diagnosing, preventing or treating diseases in which mucus is involved, e.g. cystic fibrosis, comprises a mucin-		
XX				PT	modified form, useful for diagnosing, preventing or treating diseases in which mucus is involved, e.g. cystic fibrosis, comprises a mucin-		
PI	Zhang Y, Moffatt M, Cookson W, Tinsley J;			PT	hydrolyzing activity.		
XX				XX			
DR	WPI; 2003-201405/19.			PS	Example 1; Page 33; 77pp; English.		
XX				XX			
PT	New nucleic acid sequence comprising an ANGE, CILD8 or CILD7 mRNA, or ANGE-CILD8, ANGE-			PCR	Primers ACC70299-ACC70301 were used to isolate cDNA encoding a human mucinase, designated AMCase. This enzyme hydrolyses a mucin. The mucinase is useful in the treatment of a subject against a disease in which mucin is involved or against infection by a chitin-containing pathogen. The mucinase is useful in diagnosing, preventing or treating diseases in		
PT	their hybrid, useful for screening agents for treating IgB-mediated diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or allergic rhinitis.			CC	which mucin is involved, such as cystic fibrosis, chronic obstructive pulmonary disease, asthma, bronchitis, tuberculosis, a mucin-producing tumour, or infection by a protozoan parasite		
XX				XX	Sequence 22 BP; 4 A; 3 C; 5 G; 10 T; 0 U; 0 Other;		
PS	Disclosure; Page 408; 429pp; English.			SQ	Query Match 78.8%; Score 13.4; DB 9; Length 22; Best Local Similarity 53.3%; Pred. No. 4.6e+03; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;		
XX	The invention relates to a novel isolated or recombinant nucleic acid sequence comprising an ANGE, CILD8 or CILD7 mRNA, or ANGE-CILD8, ANGE-CILD7, CILD8-CILD7, or ANGE-CILD8-CILD7 hybrid mRNA sequence, its complement, homologue or fragment. The novel nucleic acid sequences have the following activities: antiallergic, anti-asthmatic, dermatological, anti-pyretic, and anti-inflammatory. The nucleic acids of the invention may be used in gene therapy to treat disorders. The nucleic acid sequences are useful for screening agents that inhibit or enhance activity of an ANGE, CILD8 or CILD7 gene. The agent or antibody is useful for treating IgB-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic dermatitis, allergic rhinitis or non-atopic asthma. The antibody is useful in an assay detecting or measuring the polypeptide in the sample. The host cell is useful for producing, regulating and analyzing the polypeptide. The splice variant of ANGE, CILD8, or CILD7 is useful for diagnosing an IgB-mediated disease, atopy, a form of atopic disease or non-atopic asthma, or predicting the severity, or predisposition to a disease. This polynucleotide sequence represents a primer used in the exemplification of the invention.			DB	8 CTGATTTATGCGAG 22		
CC				Db			
CC				RESULT 13			
CC				ID	ADG16067/C		
CC				ID	ADG16067 standard		
CC				AC	ADG16067;		
CC				XX			
CC				DT	26-FEB-2004 (first entry)		
CC				XX			
CC				DB	PQQGDH mutagenic PCR primer SEQ ID NO:17.		
CC				XX			
SQ	Sequence 19 BP; 7 A; 6 C; 2 G; 4 T; 0 U; 0 Other;						
Query Match 82.4%; Score 14; DB 10; Length 19; Best Local Similarity 64.3%; Pred. No. 2.2e+03; Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;							

KW modified pyrroloquinoline quinone dependent glucose dehydrogenase;
 KW pyrroloquinoline quinone dependent glucose dehydrogenase;
 KW modified PQGDH; PQGDH; enzyme; glucose; clinical assay; food analysis;
 KW Acinetobacter baumannii; mutagenesis; PCR primer; ss.
 XX
 OS Synthetic
 OS *Acinetobacter baumannii*.
 XX
 .PN EP1367120-A2.
 XX
 PD 03-DRG-2003.
 XX
 PR 27-MAY-2003; 2003EP-00011930.
 XX
 PR 27-MAY-2002; 2002JP-00152911.
 XX
 PR 27-MAY-2002; 2002JP-00152913.
 XX
 PR 24-MAR-2003; 2003JP-00080244.
 XX
 PR 24-MAR-2003; 2003JP-00080310.
 XX
 PA (TOYM) TOKO BOSEKI KK.
 XX
 PI Takeshima S, Sogabe A, Oka M;
 XX
 DR WPI; 2004-063970/07.
 XX
 PT New modified pyrroloquinolone dependent glucose dehydrogenase having less
 PT activity on disaccharides and/or greater stability than wild-type PQGDH,
 PT for measuring glucose in clinical assay or food analysis.
 XX
 PS Example 5; SEQ ID NO 17; 45pp; English.
 XX
 CC The present invention describes a modified pyrroloquinoline quinone (PQQ)
 CC dependent glucose dehydrogenase (PQGDH) having less activity on
 CC disaccharides and/or greater stability than wild-type PQGDH. Also
 CC described: (1) a gene coding for the modified PQGDH; (2) a vector
 CC containing the gene of (1); (3) a transformant transformed by the vector
 CC of (2); (4) a method of manufacturing a modified PQGDH comprises
 CC cultivating the transformation of (3); (5) a glucose assay kit comprising
 CC the modified PQGDH; and (6) a method of determining glucose
 CC concentration in a sample using the modified PQGDH. The modified PQGDH
 CC is useful for measuring glucose in clinical assay or food analysis. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 52 BP; 15 A; 6 C; 6 G; 16 T; 0 U; 9 Other;
 SQ Best Local Similarity 78.8%; Score 13.4; DB 12; Length 52;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UGAUUCAUAGCAGG 17
 :|::|::|::|||
 Db 15 TGATTGATTCAGG 1
 SQ Sequence 66 BP; 18 A; 14 C; 8 G; 23 T; 0 U; 3 Other;
 SQ Best Local Similarity 78.8%; Score 13.4; DB 2; Length 66;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UGAUUCAUAGCAGG 17
 :|::|::|::|||
 Db 54 TGATTGATTCAGG 40
 RESULT 14
 ABK61045 standard; DNA; 15 BP.
 ID ABK61045
 XX
 AC ABK61045;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DB Human CLCA1 gene enzymatic nucleic acid #5416.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcySTEINE.
 XX
 OS Homo sapiens.
 XX
 DE Human gene signature HUMGS01596.
 XX
 PN WO20021674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PR 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMSON J.

XX
 PR 11-NOV-1994; 94WO-JP001916.
 XX
 PR 12-NOV-1993; 93JP-00355504.
 XX
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 XX
 PI Matsubara K, Okubo K;
 XX
 DR WPI; 1995-206931/27.
 XX
 PT Single-stranded DNA for identifying gene signatures - isolated from 3' -
 PT directed human cDNA library that reflects relative abundance of corresp.
 PT mRNA in specific human tissues.
 XX
 PS Claim 1; Page 637; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp. double
 CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in
 CC ATN9001-T26837 and which is able to hybridise to part of human genomic
 CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
 CC obtained from 3'-directed cDNA libraries prepared from various human
 CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
 CC poly (A) as the sole primer. Since the 3'- untranslated sequence is unique
 CC with respect to all the 3'-oriented cDNAs hybridise
 CC with specific mRNAs. Each library is constructed so as to reflect
 CC accurately the relative abundance of different mRNAs in the particular
 CC tissue from which it was derived. The appearance frequency of a given GS
 CC in a cDNA library can be determined (esp. using primers and probes
 CC derived from the GS sequences) as a means of diagnosing abnormal cell
 CC function or for recognising different cell types

XX
 SQ Sequence 66 BP; 18 A; 14 C; 8 G; 23 T; 0 U; 3 Other;

Query Match 78.8%; Score 13.4; DB 2; Length 66;
 Best Local Similarity 53.3%; Pred. No. 5.1e+03; ID ABK61045
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UGAUUCAUAGCAGG 17
 :|::|::|::|||
 Db 54 TGATTGATTCAGG 40

RESULT 15
 ABK61045
 ID ABK61045 standard; DNA; 15 BP.
 XX
 AC ABK61045;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DB Human CLCA1 gene enzymatic nucleic acid #5416.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcySTEINE.
 XX
 OS Homo sapiens.
 XX
 DE Human gene signature HUMGS01596.
 XX
 PN WO20021674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PR 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMSON J.

XX
 PR 01-JUN-1995.

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Gruppe A;
 XX
 DR WPI; 2002-217145/27.
 PT Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
 PT
 XX
 PS Claim 4; Page 139; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) gene by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
 SQ sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 76.5%; Score 13; DB 6; Length 15;
 Best Local Similarity 61.5%; Pred. No. 7 2e+03; Mismatches 8; Indels 5; Matches 8; Conservative 5; Mismatches 0; Indels 0; gaps 0;
 Qv 5 ATTTTCAAGCAGG 17
 Ov 1 ::::::|:|||:
 Db 1 ATTTCATTCAGCAGG 13
 RESULT 16
 ABK56376
 ID ABK56976 standard; RNA; 17 BP.
 XX
 AC ABK56876;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DB Human CLCA1 gene enzymatic nucleic acid #1247.
 XX
 Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 DD 14-FEB-2002.
 XX
 PP 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOSYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Gruppe A;
 PI

DR XX
 PT XX
 Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
 PT XX
 PS XX
 Claim 4; Page 85; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are used as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1 where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, anti-bacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
 CC SQ Sequence 17 BP; 7 A; 2 C; 3 G; 0 T; 5 U; 0 Other;
 CC Query Match 76.5%; Score 13; DB 6; Length 17;
 CC Best Local Similarity 100.0%; Pred. No. 7.3e-03;
 CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 5 AUUAGAUAGG 17
 CC Db 1 AUUUCGUUGCKGG 13
 XX
 RESULT 17
 ABK57300 ID ABK57300 Standard; RNA; 17 BP.
 XX AC ABK57300;
 XX DT 02-JUL-2002 (first entry)
 DE Human CLCA1 gene enzymatic nucleic acid #1671.
 XX Human; chloride channel calcium activated 1; CLCA1; **as**; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; vaccination; mucokinetic; acetylcysteine.
 XX OS Homo sapiens.
 XX PN WO20021674-A2.
 XX PD 14-FEB-2002.
 XX PF 09-AUG-2001; 2001WO-US024970.
 XX PR 09-AUG-2000; 2000US-0224383P.
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SNTK) SINTER USA LLC.
 PA (TM/) THOMPSON J.
 XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PT Grue A;
 XX WPI; 2002-217145/27.

PT Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
 PT Claim 4; Page 111; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) gene by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

XX Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 76.5%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUGAUUCAGU 13
 Db 5 CGUGAUUCAGU 17

RESULT 18
 ADP9717/c
 ID ADP97171 standard; DNA; 43 BP.
 XX
 AC ADP97171;
 XX
 DT 23-SEP-2004 (first entry)

DB C. albicans specific gene, orf6_3991, knockout downstream primer.

XX Diploid fungal cell; allele; gene disruption cassette;
 KW promoter replacement; fragment; antifungal; fungicide; gene therapy;
 KW infection; Candida albicans; knockout; primer; ss.
 XX
 OS Candida albicans.
 OS unidentified.

XX WO2004056965-A2.

PD 08-JUL-2004.

XX 19-DEC-2003; 2003WO-US040618.

PR 19-DEC-2002; 2002US-0434832P.

XX (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 PI Roemer T, Jiang B, Boone C, Bussey H;
 XX
 DR WPI; 2004-500296/47.

XX Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment.

XX
 PS Claim 76; SEQ ID NO 1206; 163pp; English.

XX The invention relates to a novel method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The method comprises modifying the alleles of a gene in diploid fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment. The invention further comprises: assembling a collection of diploid fungal cells each of which comprises modified alleles of a different gene; a strain of diploid fungal cells comprising inactivated alleles of a gene, where the first allele of the gene is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene, and where the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid strains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to a target nucleotide sequence comprising any of the 310 nucleotide sequences listed in the specification (ADP98516-ADP98825); identifying a gene that is essential to the survival or growth of a fungus, that contributes to the virulence and/or pathogenicity of a fungus, or that contributes to the resistance of a diploid fungus to an antifungal agent; identifying an antifungal agent that inhibits the growth of a diploid fungus, or a therapeutic agent for treatment of a mammalian disease; correlating changes in the levels of proteins or gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell; a purified or isolated nucleic acid molecule comprising a nucleotide sequence encoding a gene product required for proliferation of Candida albicans, where the gene product consists of any of the above-mentioned amino acid sequences; a vector comprising a promoter operably linked to the nucleic acid molecule cited above; a host cell containing the vector; a purified or isolated polypeptide comprising any of the 61 amino acid sequences given in the specification (ADP96718-ADP96778); a fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, the fragment consisting of at least 6 consecutive residues of any of ADP9826-ADP99135 ; producing a polypeptide; identifying a compound which modulates the activity of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825; eliciting an immune response in an animal; a strain of Candida albicans, where a first allele of a gene comprising any of ADP98516-ADP98825 is inactive and a second allele of the gene is under control of a heterologous promoter; identifying a compound or binding partner that binds to the polypeptide comprising any of ADP9826-ADP99135, or its fragment; identifying a compound having the ability to inhibit growth or proliferation of Candida albicans; inhibiting growth or proliferation of Candida albicans cells; manufacturing an antimycotic compound; treating an infection of a subject by Candida albicans; preventing or containing contamination of an object by Candida albicans, or for preventing or inhibiting formation on a surface of a biofilm comprising Candida albicans; a pharmaceutical composition comprising a therapeutic amount of an agent which reduces the activity or level of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825 in a pharmaceutical carrier; an antibody preparation which binds the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP9826-ADP99135, a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicidal activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This polynucleotide sequence represents a knockout primer used in the exemplification of the

CC invention. NOTE: This sequence was downloaded from an electronic sequence
 CC listing provided on the WIPO website.
 XX sequence 43 BP; 19 A; 7 C; 5 G; 12 T; 0 U; 0 Other;
 SQ Best Local Similarity 53.8%; Score 13; DB 12; Length 43;
 Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCGUGAUUCAGT 13
 Db 22 CCTGAAATTCACTG 10

RESULT 19

ABN45930 Standard; DNA; 60 BP.
 ID ABN45930
 XX AC ABN45930;
 XX AC ABN45930;
 DT 15-JUL-2002 (first entry)

DB Human spliced transcript detection oligonucleotide SEQ ID NO:18678.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200210449-A2.
 XX PD 07-FEB-2002.
 XX PP 20-JUL-2001; 2001WO-IB001903.
 XX PR 28-JUL-2000; 2000US-0221607P.
 XX PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX DR WPI; 2002-257583/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

XX PS Example 1; SEQ ID NO 18678; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNA that populate a (sub-)transcriptome, where the (sub-)
 CC transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, human and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 part of the printed specification, but was obtained in electronic format

RESULT 20

AAV51603 Standard; DNA; 20 BP.
 ID AAV51603
 XX AC AAV51603;
 XX AC AAV51603;
 DT 02-FEB-1999 (first entry)

DE Zea mays genome forward PCR primer #203.

XX Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.
 XX OS Synthetic.
 OS Zea mays.
 PN WO924796A1.
 XX PD 11-JUN-1998.
 XX PP 01-DEC-1997; 97WO-US021782.
 XX PR 02-DEC-1996; 96US-0032069P.
 XX PR 07-MAR-1997; 97US-00813507.
 XX PA (AFFY-) AFFYMATRIX INC.

PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
 XX DR WPI; 1998-333252/29.

XX PT Brassica species allele-specific oligonucleotide probes and primers -
 PT useful for plant breeding.

XX PS Example 1; Page 53; 65pp; English.

XX AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution of
 CC an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a back-
 CC crossed plant with an ancestral plant

SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 20;
 Best Local Similarity 56.2%; Pred. No. 9.4e+03;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCGUAGUUCAUGCAG 16
 Db 2 CTTGATTCATGCAG 17

RESULT 21

AAV51602 Standard; DNA; 23 BP.

ID AAV51602

XX AAV51602;
 AC PF
 XX XX
 DT 02-FEB-1999 (first entry)
 XX DB zea mays genome forward PCR primer #202.
 KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.
 XX OS Synthetic.
 OS Zea mays.
 XX PT
 XX PN WO9824796-A1.
 XX PD 11-JUN-1998.
 XX PR 01-DEC-1997; 97WO-US021782.
 XX PR 02-DEC-1996; 96US-0032069P.
 XX PR 07-MAR-1997; 97US-00813507.
 XX PA (AFFY-) AFFYMETRIX INC.
 XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX PS Claim 1; SEQ ID NO 108838; spp; English.
 XX PT Lemieux B, Landry BS, Sapolisky RJ, Murigneux A;
 XX DR WPI; 1998-333252/29.
 XX PT Brassica species allele-specific oligonucleotide probes and primers -
 PT useful for plant breeding.
 XX PS Example 1; Page 53; 65pp; English.
 CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution of
 CC an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a back-
 CC crossed plant with an ancestral plant
 XX SQ sequence 23 BP; 5 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 2; Length 23;
 Best Local Similarity 55.2%; Pred. No. 9.5e-03; Mismatches 9; Conservativeness 5; Indels 0; Gaps 0;
 Matches 2; Qy 1 CCUGAATTCATGCGAG 16
 Db 5 CTGTGATTCATGGCAG 20
 RESULT 22
 ACK08857
 ID ACK08857 standard; DNA; 25 BP.
 XX AC
 XX AC ACK08857;
 XX DT 14-OCT-2003 (first entry)
 XX DB Human microarray DNA oligonucleotide SEQ ID NO 108838.
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 108838.
 XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX OS Homo sapiens.
 XX PN US2003104410-A1.
 XX PD 05-JUN-2003.
 XX PT
 XX PR 15-MAR-2002; 2002US-00098263.
 XX DR 16-MAR-2001; 2001US-0276759P.
 XX PA (AFFY-) AFFYMETRIX INC.
 XX PT Mittmann MP;
 XX PI WPI; 2003-567953/53.
 XX PS
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in, in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX SQ Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 9; Length 25;
 Best Local Similarity 56.2%; Pred. No. 9.5e+03; Mismatches 9; Conservativeness 5; Indels 0; Gaps 0;
 Matches 2; Qy 1 CCUGAATTCATGCGAG 16
 Db 9 CCAGATTCTATGGAG 24
 RESULT 23
 ABK33718/C
 ID ABK33718 standard; DNA; 32 BP.
 XX AC ABK33718;
 XX DT 08-MAY-2002 (first entry)
 XX DB S. pneumoniae BVH-3 gene, PCR primer RAMJ 359.
 XX KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia;
 KW streptococcal bacterial infection; PCR; primer; ss.
 OS Streptococcus pneumoniae.
 XX PN WO200198334-A2.
 XX PD 27-DEC-2001.
 XX PN US2003104410-A1.
 XX PF 19-JUN-2001; 2001WO-CA000908.
 XX

PR 20-JUN-2000; 2000US-021683P.
 XX
 PA (SHIR-) SHIRE BIOCHEM INC.
 XX
 PI HameL J., Ouellet C., Charland N., Martin D., Brodeur B;
 XX DR WPI; 2002-122272/16.
 XX PT New Streptococcus pneumoniae BWH-3 and BWH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteremia.
 XX PS Example 1; Page 33; 113pp; English.

XX CC The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumoniae protein BWH-3, BWH-11, variants of BWH-3 or comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteremia or pneumonia infection in an individual susceptible to those disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A streptococci such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunization techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumoniae nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a primer used for the isolation of S. pneumoniae genes from which the antigenic peptides of the invention are derived.

XX SQ Sequence 32 BP; 9 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

Query Match	75.3%	Score	12.8	DB	6	Length	32
Best Local Similarity	56.2%	Pred. No.	9.8e+03				
Matches	9	Conservative	5	Mismatches	2	Indels	0
Gaps	0						

XX DB QY 2 CUGAGATTCATGCGAG 17
 24 CTGATTTCATAAGGGG 9

RESULT 24 AAV50992
 ID AAV50992 standard; DNA; 41 BP.
 XX AC AAV50992;
 XX DT 04-JAN-1999 (first entry)

XX DB Maize polymorphic marker S43G2/G6-2B DNA.

XX KW Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

XX OS Zea mays.

XX PH variation 2¹
 FT variation Location/Qualifiers
 FT /tag= a
 FT /replace= g
 FT /note= "polymorphism"

XX PN WO9824796-A1.

XX PD 11-JUN-1998.

XX PP 01-DEC-1997; 97MO-US021782.

XX PR 02-DEC-1996; 96US-0032069P.

XX PR 07-MAR-1997; 97US-00813507.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Lemieux, B., Landry BS, Sapolsky RJ, Murgneux A;

XX DR WPI; 1998-333252/29.

XX PT Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding.

XX PS Claim 1; Page 43; 65pp; English.

XX CC This DNA sequence is a region of a Zea mays genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridization, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant.

XX SQ Sequence 41 BP; 9 A; 10 C; 14 G; 8 T; 0 U; 0 Other;

Query Match	75.3%	Score	12.8	DB	2	Length	41
Best Local Similarity	56.2%	Pred. No.	1e+04				
Matches	9	Conservative	5	Mismatches	2	Indels	0
Gaps	0						

XX DB QY 1 CCTGAGATTCATGCGAG 16
 1 CTTGAATGCAATGCG 16

RESULT 25 AAV50971
 ID AAV50971 standard; DNA; 41 BP.

XX AC AAV50971;

XX DT 04-JAN-1999 (first entry)

XX DB Maize polymorphic marker S43G2/G6-2B DNA.

XX KW Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

XX OS Zea mays.

XX PH variation 2¹
 FT variation Location/Qualifiers
 FT /tag= a
 FT /replace= g
 FT /note= "polymorphism"

XX PN WO9824796-A1.

XX PD 11-JUN-1998.

XX PP 01-DEC-1997; 97MO-US021782.

XX PR 02-DEC-1996; 96US-0032069P.

XX PR 07-MAR-1997; 97US-00813507.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Lemieux, B., Landry BS, Sapolsky RJ, Murgneux A;

XX DR WPI; 1998-333252/29.

XX PT Brassica species allele-specific oligonucleotide probes and primers -

PS PT useful for plant breeding.

XX CC Claim 1; Page 43; 65pp; English.

CC CC This DNA sequence is a region of a *Zea mays* genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

SQ Sequence 41 BP; 10 A; 10 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41; Best Local Similarity 56.2%; Pred. No. 1e+04; 2; Indels 0; Gaps 0; Matches 9; Conservative 5; Mismatches 2; Idents 0; Gaps 0;

Oy 1 CCUGAUNCAUUCGAG 16

Db 1 CTGATTCATGCAG 16

RESULT 26

ID AAV50981

AAV50981 standard; DNA; 41 BP.

AC XX

XX AC AAV50984

XX ID AAV50984 standard; DNA; 41 BP.

XX AC AAV50994;

XX DT 04-JAN-1999 (first entry)

XX DT 04-JAN-1999 (first entry)

DB Maize polymorphic marker S43G1/G3-1 DNA.

KW Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

XX DB Maize polymorphic marker S43G1/G3-1 DNA.

KW Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

XX OS Zea mays.

XX PH Location/Qualifiers

XX FT variation 21

FT /tag= a

FT /replace= g

FT /note= "polymorphism"

XX PN W09824796-A1.

XX PR 02-DEC-1996; 96US-0032069P.

XX PR 07-MAR-1997; 97US-00813507.

XX PA (AFFY-) AFFYMATRIX INC.

XX PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;

XX DR WPT; 1998-333252/29.

XX PT Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding.

XX PS Claim 1; Page 43; 65pp; English.

XX CC This DNA sequence is a region of a *Zea mays* genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

XX SQ Sequence 41 BP; 8 A; 9 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41; Best Local Similarity 56.2%; Pred. No. 1e+04; 2; Indels 0; Gaps 0; Matches 9; Conservative 5; Mismatches 2; Idents 0; Gaps 0;

Oy 1 CCUGAUNCAUUCGAG 16

Db 19 CTGATTCATGCAG 34

RESULT 27

ID AAV50994

AAV50994 standard; DNA; 41 BP.

XX AC AAV50994;

XX DT 04-JAN-1999 (first entry)

DB Maize polymorphic marker S43G1/G3-1 DNA.

KW Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

XX OS Zea mays.

XX PH Location/Qualifiers

XX FT variation 21

FT /tag= a

FT /replace= g

FT /note= "polymorphism"

XX PN W09824796-A1.

XX PR 02-DEC-1996; 96US-0032069P.

XX PR 07-MAR-1997; 97US-00813507.

XX PA (AFFY-) AFFYMATRIX INC.

XX PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;

XX DR WPT; 1998-333252/29.

XX PT Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding.

XX PS Claim 1; Page 43; 65pp; English.

XX CC This DNA sequence is a region of a *Zea mays* genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

XX SQ Sequence 41 BP; 8 A; 9 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41; Best Local Similarity 56.2%; Pred. No. 1e+04; 2; Indels 0; Gaps 0; Matches 9; Conservative 5; Mismatches 2; Idents 0; Gaps 0;

AAV47798
 ID AAV47798 standard; DNA; 41 BP.
 XX
 AC AAV47798;
 XX
 DT 27-AUG-2003 (revised)
 XX
 DE Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.
 XX
 KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KW polymorphic site; corn; gramineae species; ss.
 XX
 KW Synthetic.
 OS
 OS Zea.
 XX
 PN WO9830717-A2.
 XX
 PD 16-JUL-1998.
 XX
 PP 02-DEC-1997; 97WO-EP007134.
 XX
 PR 02-DEC-1996; 96US-0032069P.
 XX
 PA (BIOC-) BIOCEN SA.
 XX
 PT Murigneux A;
 XX
 DR WPI; 1998-399160/34.
 XX
 PT Vegetal sequences including single nucleotide polymorphism - useful, e.g. to determine polymorphisms in plants, determine strain in plant breeding and to correlate polymorphisms with phenotypic traits.
 XX
 PS Claim 2; Page 13; 32pp; English.

CC The present invention describes a nucleic acid segment comprising at least 10 contiguous nucleotides from a vegetal sequence including a polymorphic site which is a single nucleotide polymorphism (SNP), or the complement of the segment. Also described are: (1) an allele-specific oligonucleotide hybridising to segment, or their complements, and (2) a method of analysing nucleic acids from a subject, by determining if a base is occupying any one (or a set) of polymorphic sites in 261 sequences derived from six maize lines (See AAV47701 to AAV47961). The segments are useful in fingerprint analysis in plants to determine which polymorphisms are present, which strain a plant belongs to and to distinguish between strains. The polymorphisms may correlate with phenotypic traits (e.g. plant growth rate or crop yield), and the segments are useful to determine the presence/absence of specific polymorphisms correlating with the existence/absence of particular traits. The segments are also useful in marker assisted back-cross techniques to select plants with a higher percentage of recurrent parent polymorphisms. The segments are also useful in marker assisted back-cross techniques to select plants with a higher percentage of recurrent parent polymorphisms. The segments incorporate SNPs which occur more frequently than other polymorphism types and are therefore more likely to be located close to genetic loci of interest; different forms of characterised SNPs are also often easier to detect than other polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41;
 Best Local Similarity 56.2%; Pred. No. 1e+04; Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCUGAUUCAUUGCAG 16
 Db 1 CTTGATTGCAATGCGAG 16

RESULT 30
 AAV47788
 ID AAV47788 standard; DNA; 41 BP.
 AC AAV47788;
 XX
 DT 27-AUG-2003 (revised)

AC AAV47809;
 XX
 DT 27-AUG-2003 (revised)
 DT 14-OCT-1998 (first entry)

XX
 DE Maize polymorphic site oligonucleotide marker Wx1-G1/G4-1.
 XX
 KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KW polymorphic site; corn; gramineae species; ss.
 XX
 OS Synthetic.
 OS Zea.
 XX
 PN WO9830717-A2.
 XX
 PD 16-JUL-1998.
 XX
 PP 02-DEC-1997; 97WO-EP007134.
 XX
 PR 02-DEC-1996; 96US-0032069P.
 XX
 PA (BIOC-) BIOCEN SA.
 XX
 PT Murigneux A;
 XX
 DR WPI; 1998-399160/34.
 XX
 PT Vegetal sequences including single nucleotide polymorphism - useful, e.g. to determine polymorphisms in plants, determine strain in plant breeding and to correlate polymorphisms with phenotypic traits.
 XX
 PS Claim 2; Page 13; 32pp; English.

CC The present invention describes a nucleic acid segment comprising at least 10 contiguous nucleotides from a vegetal sequence including a polymorphic site which is a single nucleotide polymorphism (SNP), or the complement of the segment. Also described are: (1) an allele-specific oligonucleotide hybridising to segment, or their complements, and (2) a method of analysing nucleic acids from a subject, by determining if a base is occupying any one (or a set) of polymorphic sites in 261 sequences derived from six maize lines (See AAV47701 to AAV47961). The segments are useful in fingerprint analysis in plants to determine which polymorphisms are present, which strain a plant belongs to and to distinguish between strains. The polymorphisms may correlate with phenotypic traits (e.g. plant growth rate or crop yield), and the segments are useful to determine the presence/absence of specific polymorphisms correlating with the existence/absence of particular traits. The segments are also useful in marker assisted back-cross techniques to select plants with a higher percentage of recurrent parent polymorphisms. Segments incorporate SNPs which occur more frequently than other polymorphism types and are therefore more likely to be located close to genetic loci of interest; different forms of characterised SNPs are also often easier to detect than other polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41;
 Best Local Similarity 56.2%; Pred. No. 1e+04; Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCUGAUUCAUUGCAG 16
 Db 1 CTTGATTGCAATGCGAG 16

RESULT 30
 AAV47788
 ID AAV47788 standard; DNA; 41 BP.
 AC AAV47788;
 XX
 DT 27-AUG-2003 (revised)

RESULT 29
 AAV47809
 ID AAV47809 standard; DNA; 41 BP.
 XX

DT 14-OCT-1998 (first entry)
 XX DE Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.
 XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 XX KW polymorphic site; corn; gramineae species; ss.
 XX OS Synthetic.
 XX OS zea.
 XX PN WO9830717-A2.
 XX PD 16-JUL-1998.
 XX PF 02-DEC-1997; 97WO-EP007134.
 XX PR 02-DEC-1996; 96US-0032069P.
 XX PA (BIOC-) BIOCEN SA.
 XX PI Murigneux A.;
 XX DR WPI; 1998-399160/34.
 XX PT Vegetal sequences including single nucleotide polymorphism - useful, e.g. to determine polymorphisms in plants, determine stain in plant breeding and to correlate polymorphisms with phenotypic traits.
 XX PS Claim 2; Page 13; 32pp; English.
 CC The present invention describes a nucleic acid segment comprising at least 10 contiguous nucleotides from a vegetal sequence including a polymorphic site which is a single nucleotide polymorphism (SNP), or the complement of the segment. Also described are: (1) an allele-specific oligonucleotides hybridising to segment, or their complements, and (2) a method of analysing nucleic acids from a subject, by determining if a sequence is occupying any one (or a set) of polymorphic sites in 261 sequences derived from six maize lines (see AAV4701 to AAV47961). The segments are useful in fingerprint analysis in plants to determine which polymorphisms are present, which strain a plant belongs to and to distinguish between strains. The polymorphisms may correlate with phenotypic traits (e.g. plant growth rate or crop yield), and the polymorphisms are useful to determine the presence/absence of specific traits. The segments are also useful in marker assisted back-cross techniques to select plants with a higher percentage of recurrent parent in a back-cross population. Segments incorporate SNPs which occur more frequently than other polymorphism types and are therefore more likely to be located close to genetic loci of interest; different forms of characterised SNPs are also often easier to detect than other polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 41;
 CC Best Local Similarity 56.2%; Pred. No. 1e+04; Mismatches 5;保守性 5; Matches 9; Indels 0; Gaps 0;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 XX SQ Sequence 63 BP; 18 A; 17 C; 7 G; 21 T; 0 U; 0 Other;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 XX SQ Sequence 63 BP; 18 A; 17 C; 7 G; 21 T; 0 U; 0 Other;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;

RESULT 31
 ID AAH86424-C
 AC AAH86424 standard; DNA; 63 BP.
 XX DT 27-FEB-2002 (first entry)
 XX DB Human single nucleotide polymorphism containing DNA sequence #1281.

RESULT 32
 ID AA127809-C
 AC AA127809
 XX DT 12-OCT-2001 (first entry)
 XX DB Probe #17742 for gene expression analysis in human cervical cell sample.
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX OS Homo sapiens.
 XX PN WO0015278-A2.

KW Biallelic marker; polymorphism; human disease; diagnosis; treatment; phenotypic trait; gene therapy; forensic; paternity; mapping; cancer; transgenic; single nucleotide polymorphism; SNP; ss.
 XX OS Homo sapiens.
 XX PH Key variation Location/Qualifiers
 FT replace(20,C) /tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX PN WO9953095-A2.
 XX PD 21-OCT-1999.
 XX PF 30-MAR-1999; 99WO-US006893.
 XX PR 09-APR-1998; 98US-00057871.
 XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PI Lander ES, Wang D, Hudson T;
 XX DR WPI; 1999-620443/53.
 XX PT Polymorphic human genomic sequences and related allele-specific probes and primers, useful for genetic analysis, e.g. diagnosis and monitoring of disease.
 XX PS Claim 1; Page 168; 330pp; English.
 CC This invention describes novel human nucleic acid segments (I) containing polymorphic sites. The polynucleotides of (I) are used for, e.g. correlating disease polymorphisms (or disease susceptibility) or other phenotypic traits (e.g. baldness, obesity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation, heart or central nervous system diseases; detecting susceptibility to microbial infection; treating or preventing such diseases; forensic analysis; gene therapy; paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning of the genes responsible); and the production of transgenic organisms. Antibodies raised against (I) are useful as diagnostic and therapeutic tools and in drug screening. AAH8514 - AAH87644 represent the human DNA sequence containing biallelic polymorphic sites described in the invention
 XX SQ Sequence 63 BP; 18 A; 17 C; 7 G; 21 T; 0 U; 0 Other;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;
 CC Query Match 75.3%; Score 12.8; DB 2; Length 63;
 CC Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 8;保守性 6; Matches 7; Indels 0; Gaps 0;

CC producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders

SQ sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04; Pred. No. 1.1e+04; Mismatches 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUUCAUUCAGG 17
Db 57 CTGATTCATTCTAGG 42

RESULT 35
ID ABA40677/C
ABA40677 standard; DNA; 80 BP.

AC ABA40677;
XX DT 23-JAN-2002 (first entry)

DB Probe #19143 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; SS.
OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PP 30-JAN-2001; 2001WO-US000666.

XX PR 0-4-FEB-2000; 2000US-0180312P.
PR 25-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0234687P.
PR 04-OCT-2000; 2000US-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PR Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 25347; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention

SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

XX Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04; Pred. No. 1.1e+04; Mismatches 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUUCAUUCAGG 17
Db 57 CTGATTCATTCTAGG 42

RESULT 36
ID AAK50790/C
AAK50790 standard; DNA; 80 BP.

AC AAK50790;
XX AC AAK50790;

XX DT 06-Nov-2001 (first entry)

DB Human bone marrow expressed single exon probe SEQ ID NO: 25347.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; melanoma; SS.
OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00532365.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0234687P.
PR 04-OCT-2000; 2000US-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 25347; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention

SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

XX Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04; Pred. No. 1.1e+04; Mismatches 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUUCAUUCAGG 17
Db 57 CTGATTCATTCTAGG 42

RESULT 37
ID AAK24792/C
AAK24792 standard; DNA; 80 BP.

AC AAK24792;
XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe SEQ ID NO: 24783.

Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04; Pred. No. 1.1e+04; Mismatches 5; Mismatches 2; Indels 0; Gaps 0;

SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW s.
 XX OS Homo sapiens.
 XX WO200157275-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000667.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-TUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-024687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488998/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-483446/52.
 XX CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in human
 CC brain samples, which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 4; Length 80;
 Best Local Similarity 56.2%; Pred. No. 1.1e+04; 2; Mismatches 5; Indels 0; Gaps 0;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CUGAUUCAUUCAGCAGG 17
 Db 57 CTGATTCGATTCAGG 42
 RESULT 3⁸
 ABS0382/C ABSS0382 standard; DNA; 80 BP.
 ID ABS24274 standard; DNA; 80 BP.
 XX AC ABS24274;
 XX DT 19-AUG-2002 (first entry)
 DB Human genome-derived single exon probe ORF from lung SEQ ID No 24265.
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; IUD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemobiseiosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 OS Homo sapiens.
 XX WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000665.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-TUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-024687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488998/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-483446/52.
 XX CC The invention relates to a single exon nucleic acid probe (SENPs) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/pct_sequences
 XX SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 4; Length 80;
 Best Local Similarity 56.2%; Pred. No. 1.1e+04; 2; Mismatches 5; Indels 0; Gaps 0;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CUGAUUCAUUCAGCAGG 17
 Db 57 CTGATTCGATTCAGG 42
 RESULT 3⁹
 ABS24274/C ABS24274 standard; DNA; 80 BP.
 ID ABS24274 standard; DNA; 80 BP.
 XX AC ABS24274;
 XX DT 19-AUG-2002 (first entry)
 DB Human genome-derived single exon probe ORF from lung SEQ ID No 24265.
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; IUD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemobiseiosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 OS Homo sapiens.
 XX WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PP 30-JAN-2001; 2001WO-US000665.

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00633366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 measure gene expression in human lung samples.

PS Claim 4; SEQ ID NO 24265; 63pp; English.

CC The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridization of detectably
 labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several
 tissues and/or cell types using hybridisation to a single exon
 microarray having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 1201 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 Pudlak syndrome, sarcodystrophy, pulmonary haemosiderosis, pulmonary
 histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,
 Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 present sequence is a single exon probe open reading frame of the
 invention. Note: The sequence data for this patent did not form part of
 the printed specification, but was obtained in electronic format directly
 from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Query Match Best Local Similarity 75.3%; Score 12.8; DB 6; Length 80;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUCAUGACGAG 17
 Db 57 CTGATGGCATTCAGG 42

AC ACDB1396;
 XX 19-SEP-2003 (first entry)
 DT XX
 DB E. coli K12 MG1655 biochip probe SEQ ID 12672.
 XX KW Biochip; gene expression; gut; diagnostic; detection; probe; ss.
 OS Escherichia coli.
 XX PN EP1260592-A1.
 XX PD 27-NOV-2002.
 XX PP 17-MAY-2001; 2001EP-00112179.
 XX PR 17-MAY-2001; 2001EP-00112179.
 XX PA (MWGB-) MWG-BIOTECH AG.
 XX PI Donner H, Drescher B, Huber A, Weber J;
 XX DR WPI; 2003-241155/24.
 XX PT Biochip containing probes complementary with open reading frames in
 Escherichia coli K12, useful for detecting gene expression and expression
 patterns.
 PS Claim 3; Page 1973; 2004pp; German.
 CC This invention describes a novel biochip comprising probe spots, each
 containing many identical probes. The probes are nucleotide sequences of
 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 least one includes a segment of at least 20 bases identical with, or
 complementary to, a segment of an open reading frame (orf) of Escherichia
 coli K12. The biochip is used for specific detection of gene expression
 in K12 and for determining the gene expression pattern, e.g. for
 diagnostic determination of which E. coli strains are present in the gut,
 and to determine the effects of e.g. growth media on gene expression. The
 biochip provides as comprehensive as possible detection of the K12
 genome, with simultaneous analysis of many different genes with a single
 device, and comparison of gene expression between K12 and its mutants or
 other E. coli strains in a single experiment. Apart from qualitative and
 quantitative information about gene expression, it also allows
 measurement of population densities for the various strains. The use of
 synthetic oligonucleotides for preparation of probes allows free
 variation in probe length and ensures high purity (and thus selectivity,
 reactivity and reproducibility); also synthetic probes are generally
 shorter than probes prepared by polymerase chain reaction. ACDB8731 to
 ACB81540 represent oligonucleotide probes used with the biochip described
 in the invention
 XX SQ Sequence 100 BP; 27 A; 21 C; 30 G; 22 T; 0 U; 0 Other;
 Query Match Best Local Similarity 75.3%; Score 12.8; DB 8; Length 100;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUCAUGACGAG 17
 Db 11 CTGATGGCATTCAGG 42

Search completed: May 13, 2005, 17:06:01
 Job time : 131.827 secs

RESULT 40
 ACDB1396
 ID ACDB1396 standard; DNA; 100 BP.

ALIGNMENTS

```

RESULT 1
US-09-396-196G-54192/c
; Sequence 54192, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396, 196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/0100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; NUMBER OF SEQ ID NOS: 127805
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-54192

Query Match 78.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 6.9e+02; Mismatches 8; Conservati
Matches 6; Indels 0; Gaps 0;
QY 3 UGAUUCAUAGCAGG 17
QY :||::||:||| 11
Db 25 TGCTTCATGGAGG 11

RESULT 2
US-09-396-196G-60898
; Sequence 60898, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/0100, 678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-60898

Query Match 78.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 6.9e+02; Mismatches 8; Conservati
Matches 6; Indels 0; Gaps 0;
QY 1 CCUGAATUCAUTGCA 15
QY :||:||:||:||| 24
Db 10 CCTGATTTCATGAA 24

RESULT 3
US-09-396-196G-119128/c
; Sequence 119128, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396, 196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/0100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; NUMBER OF SEQ ID NOS: 127805
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-119128

Query Match 76.5%; Score 13; DB 4; Length 25;
Best Local Similarity 53.8%; Pred. No. 1.1e+03; Mismatches 7; Conservati
Matches 6; Indels 0; Gaps 0;
QY 3 UGAUUCAUAGCAGG 15
QY :||:||:||| 13
Db 25 TGAATTTCATGCA 13

RESULT 4
US-09-422-978-9923/c
; Sequence 9923, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET_020CP1
; CURRENT APPLICATION NUMBER: US/09/422, 978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298, 850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 6/109, 732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 6/0/082, 614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9923
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-8287 for SEQ 2058, in compleme
; US-09-422-978-9923

Query Match 72.9%; Score 12.4; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.3e+03; Mismatches 7; Conservati
Matches 6; Indels 1; Gaps 0;
QY 1 CCTGAAATUCAUTGCA 14
QY :||:||:||:||| 7
Db 20 CCTGATTAAATGCA 7

RESULT 5
US-09-396-196G-3128/c
; Sequence 3128, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396, 196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/0100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; NUMBER OF SEQ ID NOS: 127805
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-3128

Query Match 76.5%; Score 13; DB 4; Length 25;
Best Local Similarity 53.8%; Pred. No. 1.1e+03; Mismatches 7; Conservati
Matches 6; Indels 0; Gaps 0;
QY 3 UGAUUCAUAGCAGG 15
QY :||:||:||| 13
Db 25 TGAATTTCATGCA 13

```

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; APPLICANT: David Lockhart
; INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-3128

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3129
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-3129

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 105607
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-105607

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Houghron, Alan
APPLICANT: Bartido, Shirley M.
APPLICANT: Xu, Yiquning
APPLICANT: Wang, Siqun
TITLE OF INVENTION: Method and Reagents for Genetic
TITLE OF INVENTION: Immunization
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheim & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/230,199
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/12675
 FILING DATE: 18-JULY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Marina T. Larson
 REGISTRATION NUMBER: 32,038
 REFERENCE/DOCKET NUMBER: MSK.P-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (970) 668-2050
 TELEX: (970) 688-2082
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31
 TYPE: nucleic acid
 STRANDBEADNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 HYPOTHETICAL: no
 ANTI-SENSE: no
 ;US-02-230-199-17

RESULT 10
 Query Match 72.9%; Score 12.4; DB 3; Length 31;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCUGAUUCAUGC 14
 Db 24 CCTGATATCATGC 11

US-09-365-121-10/C
 Sequence 10, Application US/09365121
 Patent No. 6297365
 GENERAL INFORMATION:
 APPLICANT: ADAMS, Christopher C.
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: SCHROTH, Gary P.
 TITLE OF INVENTION: DECOY PROBES
 CURRENT APPLICATION NUMBER: US/09/867,193
 CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: 09/365,121
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 10
 LENGTH: 49
 TYPE: DNA
 ORGANISM: synthetic construct
 ;US-09-365-121-10

Query Match 72.9%; Score 12.4; DB 3; Length 49;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 UGAUUCAUUGCAG 16
 Db 25 TGATTTCAGTGCG 12

RESULT 11
 Sequence 11, Application US/09365121
 Patent No. 6297365
 GENERAL INFORMATION:
 APPLICANT: ADAMS, Christopher C.
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: SCHROTH, Gary P.
 TITLE OF INVENTION: DECOY PROBES
 CURRENT APPLICATION NUMBER: US/09/867,193
 CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: 09/365,121
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 49
 TYPE: DNA

RESULT 12
 Sequence 10, Application US/09867193
 Patent No. 6602668
 GENERAL INFORMATION:
 APPLICANT: ADAMS, Christopher C.
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: SCHROTH, Gary P.
 TITLE OF INVENTION: DECOY PROBES
 FILE REFERENCE: US Seq. Listing
 CURRENT APPLICATION NUMBER: US/09/867,193
 CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: 09/365,121
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 10
 LENGTH: 49
 TYPE: DNA
 ORGANISM: synthetic construct
 ;US-09-867-193-10

Query Match 72.9%; Score 12.4; DB 4; Length 49;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 UGAUUCAUUGCAG 16
 Db 25 TGATTTCAGTGCG 12

RESULT 13
 Sequence 11, Application US/09867193
 Patent No. 6602668
 GENERAL INFORMATION:
 APPLICANT: ADAMS, Christopher C.
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: SCHROTH, Gary P.
 TITLE OF INVENTION: DECOY PROBES
 FILE REFERENCE: US Seq. Listing
 CURRENT APPLICATION NUMBER: US/09/867,193
 CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: 09/365,121
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 49
 TYPE: DNA

; ORGANISM: synthetic construct
US-09-867-193-11

Query Match 72.9%; Score 12.4; DB 4; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03; Length 49;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUTUCAUUGGAG 16
Db 25 TGTATTTCAGTGCGG 12

RESULT 14
US-08-199-219-2
; Sequence 2, Application US/08199219
; Patent No. 6031151
; Patent No. 6031151 5698768
; GENERAL INFORMATION:
; APPLICANT: DRAPER, JOHN
; TITLE OF INVENTION: CALLUS-SPECIFIC PROMOTERS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT RELEASE #1.0, VERSION #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,219
; FILING DATE: 01 MARCH 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB92/01602
; PRIOR APPLICATION DATA: FILING DATE: 02 SEPTEMBER 1992
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDBNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..20
; OTHER INFORMATION: /product= "IPCR 1 PRIMER"
; US-08-199-219-2

Query Match 71.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 52.9%; Pred. No. 3e+03; Length 25;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGCAGG 17
Db 2 CCTGACTTATGGCCGG 18

RESULT 15
US-09-189-653-9
; Sequence 9, Application US/09189653
; Patent No. 6171792
; GENERAL INFORMATION:
; APPLICANT: BRENT, ROGER
; APPLICANT: XU, C. WILSON
; APPLICANT: MENDELSON, ANDREW R.
; APPLICANT: LOK, WALTER L.
; TITLE OF INVENTION: DETECTION SYSTEMS FOR REGISTERING
; FILE REFERENCE: 00786/J17002
; CURRENT APPLICATION NUMBER: US/09/189,653

Query Match 71.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 3.1e+03; Length 25;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGUGAUUCAUUGCAGG 17
Db 2 CCTGAAUATTCAGGCAGG 18

RESULT 16
US-09-396-196G-75597/c
; Sequence 7, 5557, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: METHODS OF GENETIC ANALYSIS
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 75597
; LENGTH: 25

TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-75597

Query Match 71.8%; Score 12.2; DB 4; Length 25;
Best Local Similarity 58.8%; Pred. No. 3.1e+03; Length 25;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGCAGG 17
Db 23 CCTGATGACTTGGCAGG 7

RESULT 17
US-09-396-196G-75598/c
; Sequence 7, 5558, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: METHODS OF GENETIC ANALYSIS
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 75598
; LENGTH: 25

TYPE: DNA
; ORGANISM: mus musculus

US-09-396-196G-7559B

Query Match 71.8%; Score 12.2; DB 4; Length 25;

Best Local Similarity 58.8%; Pred. No. 3.1e+03; Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccugauucuauugcagg 17
 Db 17 CCTGATTTGATTCAAGG 1

RESULT 18
 US-09-245-041-60/c
 Sequence 60, Application US/09245041
 Patent No. 6274339

GENERAL INFORMATION:

APPLICANT: More, K.

APPLICANT: Nagle, D.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY

FILE REFERENCE: 7853-136

CURRENT APPLICATION NUMBER: US/09/245,041

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/093,630

EARLIER FILING DATE: 1998-07-21

EARLIER APPLICATION NUMBER: 60/104,978

EARLIER FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 131

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 60

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

US-09-245-041-60

RESULT 19
 US-09-358-055B-61/c
 Sequence 61, Application US/09358055B
 Patent No. 6713277

GENERAL INFORMATION:
 APPLICANT: Moore, K.

APPLICANT: Nagle, D.L.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS INCLUDING OBESITY

FILE REFERENCE: 7853-151

CURRENT APPLICATION NUMBER: US/09/358,055B

CURRENT FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: 09/245,041

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 153

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 61

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Primer

US-09-893-238-60

Query Match 71.8%; Score 12.2; DB 4; Length 26;
 Best Local Similarity 52.9%; Pred. No. 3.1e+03; Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccugauucuauugcagg 17
 Db 21 CCTGATTTGATTCAAGG 5

RESULT 20
 US-09-893-238-60/c
 Sequence 60, Application US/09893238

GENERAL INFORMATION:

APPLICANT: Moore, K.

APPLICANT: Nagle, D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

FILE REFERENCE: 7853-237

CURRENT APPLICATION NUMBER: US/09/893, 238

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: 09/245, 041

PRIOR FILING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: 60/093, 630

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 129

SOFTWARE: FastSBQ for Windows Version 3.0

SEQ ID NO 60

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Primer

US-09-893-238-60

Query Match 71.8%; Score 12.2; DB 4; Length 26;
 Best Local Similarity 52.9%; Pred. No. 3.1e+03; Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccugauucuauugcagg 17
 Db 21 CCTGATTTGATTCAAGG 5

RESULT 21
 US-09-426-776A-8

Sequence 8, Application US/09426776A
 Patent No. 6733937

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

APPLICANT: Lam, Tong Jin

TITLE OF INVENTION: SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS

FILE REFERENCE: 1781-0178P

CURRENT APPLICATION NUMBER: US/09/426,776A

CURRENT FILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Version 3.0

SEQ ID NO 8

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: BamGal forward primer with BamHI restriction site and some beta-

OTHER INFORMATION: Primer

US-09-358-055B-61

Query Match 71.8%; Score 12.2; DB 4; Length 26;
 Best Local Similarity 52.9%; Pred. No. 3.1e+03; Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccugauucuauugcagg 17

Qy 1 ccugauucuauugcagg 17

Db 21 CCTGATTTGATTCAAGG 5

RESULT 20

US-09-893-238-60/c

Sequence 60, Application US/09893238

Patent No. 6727348

GENERAL INFORMATION:

APPLICANT: Moore, K.

APPLICANT: Nagle, D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND

DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

FILE REFERENCE: 7853-237

CURRENT APPLICATION NUMBER: 60/093, 630

PRIOR FILING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: 60/104, 978

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 129

SOFTWARE: FastSBQ for Windows Version 3.0

SEQ ID NO 60

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Primer

US-09-893-238-60

Query Match 71.8%; Score 12.2; DB 4; Length 26;

Best Local Similarity 47.1%; Pred. No. 3.2e+03; Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccugauucuauugcagg 17

Db 11 CGTGATTCTGGTGGCCG 27

RESULT 22
US-09-396-196G-108816/C
; Sequence 108816, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 108816
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-108816

RESULT 23
US-09-422-978-3740/C
; Sequence 3740, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenthal, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET_020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/238,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO: 3740
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-10307-115 : polymorphic base A or G
; US-09-422-978-3740

Query Match 70.6%; Score 12; DB 4; Length 25;
Best Local Similarity 58.3%; Pred. No. 4e+03; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUUCAUGCGGG 17
Db 16 TTTCATGTGAGG 5

RESULT 24
US-09-513-999C-15276
; Sequence 15276, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; APPLICANT: Dumas Milne Edwards, J.B.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/122,487
; CURRENT FILING DATE: 1999-02-26
; PRIORITY FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 15276
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-15276

Query Match 70.6%; Score 12; DB 4; Length 57;
Best Local Similarity 58.3%; Pred. No. 4.6e+03; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUUCAUGCGGG 17
Db 4 TTTCATGTGAGG 15

RESULT 25
US-09-073-567-11/C
; Sequence 11, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiandong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruilwen Zhang
; TITLE OF INVENTION: MDRI-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: .Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 98,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; MOLECULE TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; HYPOTHETICAL: NO

;

US-09-073 567-11 NO

Query Match 69.4%; Score 11.8; DB 3; Length 20;
Best Local Similarity 46.7%; Pred. No. 4.9e+03;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUCAUUGCAGG 17
Db 16 TCATTCATGCGATG 2

RESULT 26

US-09-073-567-34

; Sequence 34, Application US/09073567

; Patent No. 6013786

; GENERAL INFORMATION:

; APPLICANT: Jiandong Chen

; APPLICANT: Sudhir Agrawal

; APPLICANT: Ruilwen Zhang

TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive, 32nd Floor

STATE: IL

CITY: Chicago

ZIP: 60606

CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 97

APPLICATION NUMBER: US/09/073,567

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Greenfield, Michael S.

REGISTRATION NUMBER: 37,147

REFERENCE/DOCKET NUMBER: 98,057-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 913-0001

TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 157:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base Pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-09-280-805-157

Query Match 69.4%; Score 11.8; DB 3; Length 20;
Best Local Similarity 46.7%; Pred. No. 4.9e+03;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUCAUUGCAGG 17
Db 1 TCATTCATGCGATG 15

RESULT 28

US-08-811-492-53

Sequence 53, Application US/08811492

; Patent No. 583247

; GENERAL INFORMATION:

; APPLICANT: COMB, DONALD G.

; APPLICANT: PERLER, FRANCINE B.

; APPLICANT: JACK, WILLIAM E.

; APPLICANT: XU, MING-QUN

; APPLICANT: HODGES, ROBERT A.

; APPLICANT: NORN, CHRISTOPHER J.

; APPLICANT: CHONG, SHARONG S.C.

; APPLICANT: ADAM, ERIC

; APPLICANT: SOUTHWORTH, MAURICE

TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR PRODUCTION AND METHODS FOR PURIFICATION OF TARGET PROTEINS

NUMBER OF SEQUENCES: 155

CORRESPONDENCE ADDRESS:

ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.

STREET: 32 TOZER ROAD

CITY: BEVERLY

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 01915

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

RESULT 27

US-09-280-805-157

; Sequence 157, Application US/09280805

; Patent No. 6184212

GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.

APPLICANT: Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: PCT/US96/10545A
 CURRENT APPLICATION DATE:
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION:
 CURRENT APPLICATION NUMBER: US/08/811,492
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/580,555
 CURRENT FILING DATE: 29-DEC-1995
 CURRENT CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/146,885
 CURRENT FILING DATE: 03-NOV-1993
 CURRENT CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/004,139
 CURRENT FILING DATE: 09-DEC-1992
 CURRENT CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Gregory D
 REGISTRATION NUMBER: 30901
 REFERENCE/DOCKET NUMBER: NBB-036C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 508-927-5054
 TELEX: 508-927-1705
 FAX: 508-927-5054
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-811-492-53

Query Match 69.4%; Score 11.8; DB 2; Length 21;
 Best Local Similarity 60.0%; Pred. No. 4.9e+03; 9; Mismatches 4; Indels 2; Gaps 0;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	Db
1 CCUGAUUCAUUGCA 15	1 CCTGAAATTCACTGCA 15

RESULT 29
 PCT-US96-10545A-53
 Sequence 53, Application PC/TUS9610545A
 GENERAL INFORMATION:
 APPLICANT: COMB, DONALD G.
 APPLICANT: PERLER, FRANCINE B.
 APPLICANT: JACK, WILLIAM E.
 APPLICANT: XU, MING-QIN
 APPLICANT: HODGES, ROBERT A.
 APPLICANT: NORNEN, CHRISTOPHER J.
 TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
 TITLE OF INVENTION: PRODUCTION
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
 STREET: 32 TOZER ROAD
 CITY: BEVERLY
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 01915
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/002,361
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION:
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/002,361
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION:
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/002,361
 CURRENT FILING DATE:

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: PCT/US96/10545A
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION:
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/580,555
 CURRENT FILING DATE: 28-JUN-1995
 CURRENT CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/146,885
 CURRENT FILING DATE: 03-NOV-1993
 CURRENT CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US 08/004,139
 CURRENT FILING DATE: 09-DEC-1992
 CURRENT CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: WILLIAMS, GREGORY D.
 REGISTRATION NUMBER: 30901
 REFERENCE/DOCKET NUMBER: NBB-036C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 927-5054
 TELEX: (508) 927-1705
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-10545A-53

Query Match 69.4%; Score 11.8; DB 5; Length 21;
 Best Local Similarity 60.0%; Pred. No. 4.9e+03; 9; Mismatches 4; Indels 2; Gaps 0;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	Db
1 CCUGAUUCAUUGCA 15	1 CCTGAAATTCACTGCA 15

RESULT 30
 US-09-002-361-24
 Sequence 24, Application US/09002361
 Patents No. 6329516
 GENERAL INFORMATION:
 APPLICANT: Halling, Blaik
 TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
 TITLE OF INVENTION: Channels
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/002,361
 CURRENT FILING DATE:
 CURRENT CLASSIFICATION:
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/09/002,361
 CURRENT FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 TELECOMMUNICATION/DOCKET NUMBER:
 TELEPHONE: 609-520-3214
 TELEX: 609-520-3259
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-002-361-24

Query Match 69.4%; Score 11.8; DB 3; Length 24;
 Best Local Similarity 53.3%; Pred. No. 5e+03; Mismatches 5; Indels 2; Gaps 0;
 Matches 8; Conservative 5; Gaps 0;

Qy 3 UGAUUCAUAGGAGG 17
 Db 5 TGAATTCTATGGTGG 19

RESULT 31
 US-08-811-492-52/C
 ; Sequence 52, Application US/08811492
 ; Patent No. 5834247
 ; GENERAL INFORMATION:
 ; APPLICANT: CORB, DONALD G.
 ; APPLICANT: PERLER, FRANCINE B.
 ; APPLICANT: JACK, WILLIAM E.
 ; APPLICANT: XU, MING-QUN
 ; APPLICANT: HODGES, ROBERT A.
 ; APPLICANT: NORREN, CHRISTOPHER J.
 ; APPLICANT: CHONG, SHARONG S.C.
 ; APPLICANT: ADAM, ERIC
 ; APPLICANT: SOUTHWORTH, MAURICE
 TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR PRODUCTION AND METHODS FOR PURIFICATION OF TARGET PROTEINS
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 155
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
 STREET: 32 TOZER ROAD
 CITY: BEVERLY
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 01915

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC\ DOS/MS\ DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/811,492
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/580,555
 FILING DATE: 29-DEC-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/496,247
 FILING DATE: 28-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/146,885
 FILING DATE: 03-NOV-1993
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/004,139

Query Match 69.4%; Score 11.8; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 5.1e+03; Mismatches 4; Indels 2; Gaps 0;
 Matches 9; Conservative 6; Gaps 0;

Qy 1 CCGCAUUCAUAGCA 15
 Db 25 CCTGATTAGTGCA 11

RESULT 32
 US-09-396-196G-22517/C
 ; Sequence 22517, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 12806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 22517
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-396-196G-22517

Query Match 69.4%; Score 11.8; DB 4; Length 25;
 Best Local Similarity 60.0%; Pred. No. 5.1e+03; Mismatches 4; Indels 2; Gaps 0;
 Matches 9; Conservative 6; Gaps 0;

Qy 3 UGAUUCAUAGGAGG 17
 Db 20 TGATTCAGTGCAAGG 6

RESULT 33
 US-09-396-196G-49638
 ; Sequence 49638, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678

```

; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 496338
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-49638

Query Match 69.4%; Score 11.8; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 5.1e+03; Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 2; Db 0; Gaps 0;

QY      2 CUGAUUCAUUCAGCAG 16
Db      5 CTGATTTAGCTGTG 19

RESULT 34
US-09-396-196G-88078
; Sequence 88078, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 88078
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-88078

Query Match 69.4%; Score 11.8; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 5.1e+03; Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 2; Db 0; Gaps 0;

QY      3 UGAUUCAUUCAGCAGG 17
Db      7 TCATCAGTTCATTGCAGG 21

RESULT 35
US-09-396-196G-89943/C
; Sequence 89943, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 89943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-89943

RESULT 36
US-09-396-196G-89944/C
; Sequence 89944, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 89944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-89944

RESULT 37
PCT-US96-10545A-52/C
; Sequence 52, Application PC/TUS9610545A
; GENERAL INFORMATION:
; APPLICANT: COMB, DONALD G.
; APPLICANT: PERLER, FRANCINE B.
; APPLICANT: JACK, WILLIAM E.
; APPLICANT: XU, MING-QUN
; APPLICANT: HODGES, ROBERT A.
; APPLICANT: NORR, CHRISTOPHER J.
; TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10545A
; APPLICATION NUMBER: US 08/580,555
; FILING DATE: 29-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/580,555
; FILING DATE: 29-DEC-1995
; ;
```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496,247
 FILING DATE: 28-JUN-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/146,885
 FILING DATE: 03-NOV-1993
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/004,139
 FILING DATE: 09-DEC-1992
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WILLIAMS, GREGORY D.
 REGISTRATION NUMBER: 30901
 REFERENCE/DOCKET NUMBER: NBB-036C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 927-5054
 TELEX: (508) 927-1705
 TELEFAX: (508) 927-1705
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-10545A-52

Query Match 69.4%; Score 11.8; DB 5; Length 25;
 Best Local Similarity 60.0%; Pred. No. 5.1e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCGAUUCAUGCA 15
 ||::|| :||| :|||
 Db 25 CCTGGAATTCTAGTGCA 11

RESULT 38
 US-08-476-634-3/C
 Sequence 3, Application US/08476634
 ; Patent No. 5674935
 ; GENERAL INFORMATION:
 APPLICANT: Becherer, Kathleen Ann
 APPLICANT: DattaGupta, Nanibhushan
 APPLICANT: Naidu, Yathi M.
 TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
 TITLE OF INVENTION: CYTOKINE SIGNAL TRANSDUCER gp130 mRNA AS INHIBITORS OF DISEASE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gen-Probe Incorporated
 STREET: 9880 Campus Point Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PasteBQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,518
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: CBI007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-2807
 TELEX: 619-546-7929
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-10545A-52

Query Match 69.4%; Score 11.8; DB 1; Length 26;
 Best Local Similarity 53.3%; Pred. No. 5.1e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CCGAUUCAUGCA 16
 ||::|| :||| :|||
 Db 22 CTAAATTCACTGCAG 8

RESULT 39
 US-08-484-518-3/C
 Sequence 3, Application US/08484518
 ; Patent No. 5747470
 ; GENERAL INFORMATION:
 APPLICANT: Becherer, Kathleen
 APPLICANT: DattaGupta, Nanibhushan
 APPLICANT: Naidu, Yathi M.
 TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gen-Probe Incorporated
 STREET: 9880 Campus Point Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PasteBQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,518
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: CBI007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-2807
 TELEX: 619-546-7929
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-10545A-52

Query Match 69.4%; Score 11.8; DB 1; Length 26;
 Best Local Similarity 53.3%; Pred. No. 5.1e+03; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CCGAUUCAUGCA 16
 ||::|| :||| :|||
 Db 22 CTAAATTCACTGCAG 8

RESULT 40
US-08-943-834-3/c
Sequence 3, Application US/08943834

; Patent No. 5788612

GENERAL INFORMATION:

APPLICANT: Becherer, Kathleen Ann

APPLICANT: DattaGupta, Nanibushan

APPLICANT: Naidu, Yathi M.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: CYTOKINE SIGNAL TRANSDUcer SP130 mRNA AS INHIBITORS OF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gen-Probe Incorporated

STREET: 9880 Campus Point Drive

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,834

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/476,634

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Fisher, Carlos A.

REGISTRATION NUMBER: 36,510

REFERENCE/DOCKET NUMBER: C31006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-2807

TELEFAX: 619-546-7929

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

US-08-943-834-3

Query Match 69.4%; Score 11.8; DB 1; Length 26;

Best Local Similarity 53.3%; Pred. No. 5.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy	2 CGAUUCAUCAGCAG 16
Db	22 CTAATTCACGAG 8

Search completed: May 13, 2005, 18:27:23
Job time : 45.0364 SECs

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OM nucleic - nucleic search, using sw model
 Run on: May 13, 2005, 16:54:55 ; Search time 144.964 Seconds
 (without alignments)
 717.723 Million cell updates/sec

Title: US-09-927-046-143
 Perfect score: 17

Sequence: 1 ccgauaucauugcagg 17

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 562332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 5530346

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

1:	/cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*	c	12	14	82.4	19	19	US-10-481-613-159	Sequence 159, App
2:	/cgn2_6/prodata/2/pubpna/PCT1_NEW_PUB.seq:*	c	13	14	82.4	25	19	US-10-719-900-922893	Sequence 922893,
3:	/cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*	c	14	13.4	81.2	25	19	US-10-719-900-11606	Sequence 71606,
4:	/cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*	c	15	13.4	78.8	22	14	US-10-004-219B-12	Sequence 12, Appl
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6:	/cgn2_6/prodata/2/pubpna/PCUTS_PUBCOMB.seq:*	c	17	13.4	78.8	25	19	US-10-719-900-4994	Sequence 94994, A
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12:	/cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*	c	23	13.4	78.8	52	17	US-10-445-789-17	Sequence 17, Appl
13:	/cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*	c	24	13	76.5	15	10	US-09-927-046-5416	Sequence 5416, AP
14:	/cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:*	c	25	13	76.5	15	10	US-10-839-688-70	Sequence 70, Appl
15:	/cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*	c	26	13	76.5	17	10	US-09-927-046-1247	Sequence 1247, AP
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18:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	29	13	76.5	25	19	US-10-719-900-491812	Sequence 491812,
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21:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	32	13	76.5	60	10	US-09-908-975-18678	Sequence 1206, AP
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34:	/cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*	c	45	12.8	75.3	25	19	US-10-719-900-551683	Sequence 551683,
35:	/cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*	c	46	12.8	75.3	25	19	US-10-719-900-651813	Sequence 651813,
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37:	/cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*	c	48	12.8	75.3	25	19	US-10-719-900-935189	Sequence 935189,
38:	/cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*	c	49	12.8	75.3	31	18	US-10-138-674-19717	Sequence 19717, A
39:	/cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:*	c	50	12.8	75.3	31	18	US-10-719-900-24949A-19717	Sequence 19717, A
40:	/cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*	c	51	12.8	75.3	31	18	US-10-712-633-5154	Sequence 55154, AP
41:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	52	12.8	75.3	32	10	US-09-84-654-175	Sequence 173, App
42:	/cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*	c	53	12.8	75.3	70	13	US-10-027-632-177723	Sequence 177723,
43:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	54	12.8	75.3	70	13	US-10-027-632-177740	Sequence 177740,
44:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	55	12.8	75.3	70	13	US-10-027-632-177757	Sequence 177757,
45:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	56	12.8	75.3	70	13	US-10-027-632-177774	Sequence 177774,
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48:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	59	12.8	75.3	70	17	US-10-027-632-177757	Sequence 177757,
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50:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	61	12.8	75.3	80	9	US-09-864-761-25997	Sequence 25997, A
51:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	62	12.8	75.3	20	17	US-10-349-143-9923	Sequence 9923, AP
52:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	63	12.4	72.9	25	18	US-10-483-417-4	Sequence 4, Appl
53:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	64	12.4	72.9	25	19	US-10-719-900-171642	Sequence 171642,
54:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	65	12.4	72.9	25	19	US-10-719-900-318909	Sequence 318909,
55:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	66	12.4	72.9	25	19	US-10-719-900-388452	Sequence 388452,
56:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	67	12.4	72.9	25	19	US-10-719-900-501248	Sequence 501248,
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58:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	69	12.4	72.9	25	19	US-10-719-900-67687	Sequence 67687,
59:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	70	12.4	72.9	25	19	US-10-719-900-71795	Sequence 71795,
60:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	71	12.4	72.9	25	19	US-10-719-900-922629	Sequence 922629,
61:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	72	12.4	72.9	25	19	US-10-719-900-922894	Sequence 922894,
62:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	73	12.4	72.9	25	19	US-10-616-309-2	Sequence 2, Appli
63:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	74	12.4	72.9	25	19	US-10-809-189-3128	Sequence 3128, AP
64:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	75	12.4	72.9	25	19	US-10-809-189-3129	Sequence 3129, AP
65:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	76	12.4	72.9	25	19	US-10-809-189-27997	Sequence 27997, A
66:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	77	12.4	72.9	25	19	US-10-809-189-305607	Sequence 105607,
67:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	78	12.4	72.9	31	9	US-09-898-541-151	Sequence 17, Appl
68:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	79	12.4	72.9	49	9	US-09-867-193-10	Sequence 10, Appl
69:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	80	12.4	72.9	49	9	US-09-867-193-11	Sequence 11, Appl
70:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	81	12.4	72.9	49	16	US-10-375-623-10	Sequence 11, Appl
71:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	82	12.4	72.9	49	16	US-10-375-623-11	Sequence 11, Appl
72:	/cgn2_6/prodata/2/pubpna/US10_OF_PUBCOMB.seq:*	c	83	12.4	72.9	60	10	US-09-908-975-15196	Sequence 15196, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match Length	DB ID	Description
1	17	100.0	17 10 US-09-927-046-143	143	App	Sequence 143, App
2	16	94.1	17 10 US-09-927-046-142	142	App	Sequence 142, App
3	16	94.1	17 10 US-09-927-046-705	705	App	Sequence 705, App
4	15	88.2	15 10 US-09-927-046-5413	5413	App	Sequence 5413, App
5	15	88.2	15 10 US-09-927-046-5414	5414	App	Sequence 5414, App
6	15	88.2	15 10 US-09-927-046-5415	5415	App	Sequence 5415, App
7	15	88.2	17 10 US-09-927-046-141	141	App	Sequence 141, App
8	15	88.2	9 US-09-864-761-32180	32180	A	Sequence 32180, A
9	14.4	84.7	25 19 US-10-719-900-534802	534802	App	Sequence 534802, App
10	14.4	82.4	15 10 US-09-927-046-5412	5412	App	Sequence 5412, App
11	14	82.4	17 10 US-09-927-046-143	143	App	Sequence 143, App

RESULT 1
US-09-927-046-143
; Sequence 143, Application US/09927046
; Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: Ayers, Tim
APPLICANT: Grube, Andrew
APPLICANT: Szymkowiak, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric File Reference: 249/021
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927, 046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 143
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-927-046-143

Query Match 100.0%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 38; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAGCAGG 17
Db 1 CCUGAUUCAGCAGG 17

RESULT 2
US-09-927-046-142
; Sequence 142, Application US/09927046
; Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grube, Andrew
APPLICANT: Szymkowiak, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric File Reference: 249/021
CURRENT APPLICATION NUMBER: US/09/927, 046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450

Qy 1 CCUGAUUCAGCAGG 17
Db 1 CCUGAUUCAGCAGG 17

RESULT 3
US-09-927-046-705
Sequence 705, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grube, Andrew
APPLICANT: Szymkowiak, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric File Reference: 249/021
CURRENT APPLICATION NUMBER: US/09/927, 046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 705
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-927-046-705

Query Match 94.1%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 2 CUGAUUCAGCAGG 17
Db 1 CUGAUUCAGCAGG 15

RESULT 4
US-09-927-046-5413
; Sequence 5413, Application US/09927046
; Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grube, Andrew
APPLICANT: Szymkowiak, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric File Reference: 249/021
CURRENT APPLICATION NUMBER: US/09/927, 046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5413
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-927-046-5413
; Sequence 5414 Application US/09927046
; Publication No. US2003064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowiak, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927, 046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5414
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-927-046-5414
Query Match          88.2%; Score 15; DB 10; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy   1 CCUGAUUCAUUGCA 15
Db   1 CCTGATTTCATGGCA 15

RESULT 5
US-09-927-046-5414
; Sequence 141 Application US/09927046
; Publication No. US2003064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowiak, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927, 046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-927-046-41
Query Match          88.2%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 CCUGAUUCAUUGCA 15
Db   3 CCUGAUUCAUUGCA 17

RESULT 6
US-09-927-046-5415
; Sequence 5415 Application US/09927046
; Publication No. US2003064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowiak, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927, 046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-927-046-5415
; Sequence 141 Application US/09927046
; Publication No. US2003064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowiak, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927, 046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-864-761-32170
Query Match          88.2%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 CCUGAUUCAUUGCA 15
Db   3 CCUGAUUCAUUGCA 17

RESULT 8
US-09-864-761-32170
; Sequence 32170 Application US/09864761
; Patent No. US2002004873A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Beonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIORITY APPLICATION NUMBER: US 60/180,312
; PRIORITY FILING DATE: 2000-02-04
; PRIORITY APPLICATION NUMBER: US 60/207,456
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: US 09/632,366
; PRIORITY FILING DATE: 2000-08-03
; PRIORITY APPLICATION NUMBER: GB 24263.6
; PRIORITY FILING DATE: 2000-10-04
; PRIORITY APPLICATION NUMBER: US 60/236,359
; PRIORITY FILING DATE: 2000-09-27
; PRIORITY APPLICATION NUMBER: PCT/US01/00666
; PRIORITY FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00667
; PRIORITY APPLICATION NUMBER: PCT/US01/00667

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PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Ammax Sequence Listing Engine vers. 1.1
 LENGTH: 88
 SEQ ID NO 32170
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC010087.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
 OTHER INFORMATION: SWISSPROT HIT: P38650, EVALUE 6.00e-03
 OTHER INFORMATION: NT HIT: X95966.1, EVALUE 7.20e-01
 OTHER INFORMATION: EST_HUMAN HIT: AI707484.1, EVALUE 1.70e-02
 US-09-864-761-32170

Query Match 88.2%; Score 15; DB 9; Length 88;
 Best Local Similarity 60.0%; Pred. No. 5.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGCA 15
 Db 63 CCTGATTTCATGCCA 77

RESULT 9

US-10-719-900-534802/C
 Sequence 534802, Application US/10719900
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 FILE REFERENCE: 3528.1
 CURRENT APPLICATION NUMBER: US/10/719,900
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,808
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 982914
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 534802
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-10-719-900-534802

Query Match 84.7%; Score 14.; DB 19; Length 25;
 Best Local Similarity 62.5%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CUGAGUTUCAUGCAGG 17
 Db 22 CGATATCATGCGG 7

RESULT 10

US-09-927-046-5412
 Sequence 5412, Application US/09927046
 Publication No. US20030064946A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc
 APPLICANT: McSwiggen, Jim
 APPLICANT: Thompson, Jim
 APPLICANT: McKenzie, Tim
 APPLICANT: Ayers, Dave
 APPLICANT: Grube, Andrew
 APPLICANT: Szymkowski, Edmund
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric Enzyme
 FILE REFERENCE: 249/021
 CURRENT APPLICATION NUMBER: US/09/927,046
 CURRENT FILING DATE: 2001-08-09
 NUMBER OF SEQ ID NOS: 5450
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 5412
 LENGTH: 15
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-927-046-5412

Query Match 82.4%; Score 14; DB 10; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGCA 14
 Db 2 CCTGATTTCATGCCA 15

RESULT 11

US-09-927-046-144
 Sequence 144, Application US/09927046
 Publication No. US20030064946A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc
 APPLICANT: McSwiggen, Jim
 APPLICANT: Thompson, Jim
 APPLICANT: McKenzie, Tim
 APPLICANT: Ayers, Dave
 APPLICANT: Grube, Andrew
 APPLICANT: Szymkowski, Edmund
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric Enzyme
 FILE REFERENCE: 249/021
 CURRENT APPLICATION NUMBER: US/09/927,046
 CURRENT FILING DATE: 2001-08-09
 NUMBER OF SEQ ID NOS: 5450
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 144
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-09-927-046-144

Query Match 82.4%; Score 14; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAUTUCAUGCAGG 17
 Db 1 GAUTUCAUGCAGG 14

RESULT 12

US-10-481-613-159/C
; Sequence 159, Application US/10481613
; Publication No. US2005008562A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Younging
; APPLICANT: Moffatt, Miriam
; APPLICANT: Cookson, William
; APPLICANT: Tinsley, Jon
; TITLE OF INVENTION: Acetyl
; FILE REFERENCE: 16721-0003US1 / P32688WO/KWC
; CURRENT APPLICATION NUMBER: US/10/481,613
; CURRENT FILING DATE: 2003-12-19
; PRIORITY APPLICATION NUMBER: PCT/GB02/02859
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: GB 0115211.5
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: GB 0115212.3
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-10-481-613-159

Query Match 82.4%; Score 14; DB 19; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.6e+03;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAUUCAUUGCGG 17
Db 19 GATTTCATTCGG 6

RESULT 13
US-10-719-900-922893/C
; Sequence 922893, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 922893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

RESULT 15
US-10-004-219B-12
; Sequence 12, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: primer
; OTHER INFORMATION: HsAS3-A-tail
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; US-10-004-219B-12

Query Match 78.8%; Score 13.4; DB 14; Length 22;
Best Local Similarity 53.3%; Pred. No. 3.4e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CUGAUNUCAUUGCAG 16
Db 8 CTGATTTTATGCCAG 22

RESULT 16
US-10-787-845-12
; Sequence 12, Application US/10787845
; Publication No. US2004025324A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Heitz, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US

RESULT 14
US-10-719-900-716005/C
; Sequence 716005, Application US/10719900
; Publication No. US200502616A1
; GENERAL INFORMATION:

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; CURRENT APPLICATION NUMBER: US/10/787, 845
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/10/004, 219
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO: 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: primer
; FEATURE: OTHER INFORMATION: HAS3-A-tail
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; US-10-787-845-12

Query Match          78.8%; Score 13.4; DB 18; Length 22;
Best Local Similarity 53.3%; Pred. No. 3.4e+03; Matches 8; Conservative 6; Mismatches 1;
Qy      2 CUGAUUUCAUUCAGC 16
Db      8 CTGATTTATTCGAG 22
; Indels 0; Gaps 0;

RESULT 17
US-10-719-900-94994
; Sequence 94994, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 94994
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-94994

Query Match          78.8%; Score 13.4; DB 19; Length 22;
Best Local Similarity 50.0%; Pred. No. 3.5e+03; Matches 9; Conservative 5; Mismatches 1;
Qy      1 CCUGAUUUCAUUGCA 15
Db      7 CCAGATTATGCA 21
; Indels 0; Gaps 0;

RESULT 18
US-10-719-900-166732
; Sequence 166732, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 912524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-166732

Query Match          78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03; Matches 9; Conservative 5; Mismatches 1;
Qy      1 CCUGAUUUCAUUGCA 15
Db      1 CCTGATTTATTCGCA 25
; Indels 0; Gaps 0;

RESULT 21
US-10-809-189-54192/C
; Sequence 54192, Application US/10809189
; LENGTH: 25
; TYPE: DNA

```

Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIORITY APPLICATION NUMBER: US/09/396,196
; PRIORITY FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 54192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *mus musculus*
; US-10-809-189-54192

RESULT 22

Query Match 78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 53.3%; Pred. No. 3.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUUCAUUGCAGG 17
Db 25 TGCTTTCATGGCAGG 11

US-10-809-189-60898

; Sequence 60898, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIORITY APPLICATION NUMBER: US/09/396,196
; PRIORITY FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *mus musculus*
; US-10-809-189-60898

RESULT 23

Query Match 78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 53.3%; Pred. No. 3.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGCAGG 15
Db 10 CCTGATTTCATGGCAGG 24

US-10-809-189-60898

; Sequence 17, Application US/10445789
; Publication No. US20030232418A1
; GENERAL INFORMATION:
; APPLICANT: TAKESHIMA, Seiji
; APPLICANT: SOGABE, Atsushi
; APPLICANT: OKA, Masanori

RESULT 23

Query Match 78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 53.3%; Pred. No. 3.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AUUCAUUGCAGG 17
Db 1 ATTCCATGGCAGG 13

RESULT 25

Query Match 76.5%; Score 13; DB 10; Length 15;
Best Local Similarity 61.5%; Pred. No. 5.3e+03;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUUCAUUGCAGG 17
Db 1 ATTCCATGGCAGG 13

Best Local Similarity 53.8%; Pred. No. 5.7e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 6;

RESULT 30
 US-10-719-900-813289
 ; Sequence 813289, Application US/10719900
 ; Publication No. US200502614A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528_1
 ; CURRENT APPLICATION NUMBER: US/0/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIORITY APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 98294
 ; SOFTWARE: microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO: 813289
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-10-719-900-813289

Query Match 76.5%; Score 13; DB 19; Length 25;
 Best Local Similarity 53.8%; Pred. No. 5.7e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGUGAUUCATUG 13
 Qy 1 CCGUGAUUCATUG 13
 Db 12 CCTGATTCTATG 24

RESULT 31
 US-10-809-189-119128/C
 ; Sequence 119128, Application US/10809189
 ; Publication No. US200504851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101_1
 ; CURRENT APPLICATION NUMBER: US/10/809,189
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US/09/396,196
 ; PRIOR FILING DATE: 1999-09-15
 ; CURRENT APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127805
 ; SOFTWARE: FASTSEQ For Windows Version 4.0
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 ; US-10-809-189-119128

Query Match 76.5%; Score 13; DB 19; Length 25;
 Best Local Similarity 53.8%; Pred. No. 5.7e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UGAAUUCAUUGCA 15
 Qy 3 UGAAUUCAUUGCA 15
 Db 25 TGAATTCTATGCA 13

RESULT 32
 US-10-741-849-1206/c

RESULT 33
 US-09-908-975-18678
 ; Sequence 18678, Application US/09908975
 ; Publication No. US20030165843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHOSHAN, Avi
 ; APPLICANT: WASSERMAN, Alon
 ; APPLICANT: MINTZ, Eli
 ; APPLICANT: MINTZ, Liat
 ; APPLICANT: RAIGER, Simchon
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPlice \ FILE REFERENCE: 36688_005
 ; CURRENT APPLICATION NUMBER: US/09/908,975
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 60/287,724
 ; PRIOR FILING DATE: 2001-05-02
 ; PRIORITY APPLICATION NUMBER: US 60/221,607
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 32337
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 18678
 ; LENGTH: 60
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-908-975-18678

Query Match 76.5%; Score 13; DB 10; Length 60;
 Best Local Similarity 61.5%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAUUCAUUGCAG 16
 Qy 4 GAUUCAUUGCAG 16
 Db 30 GATTCTATGCG 42

RESULT 34
 US-10-751-736-12517/c
 ; Sequence 12517, Application US/10751736
 ; Publication No. US2004026520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth

; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM1.0927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 12517
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-751-736-12517

RESULT 35
Query Match 75.3%; Score 12.8; DB 18; Length 21;
Best Local Similarity 50.0%; Pred. No. 7.1e+03; Indels 0; Gaps 0;
Matches 8; Conservative 6; Mismatches 2;
Qy 2 CUGAGUTUCATUGCAGG 17
Db 18 CIGATTCCTTGTAAG 3

RESULT 35
US-10-751-736-12518/c
Sequence 12518, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM1.0927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 12518
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
; US-10-751-736-12518

Query Match 75.3%; Score 12.8; DB 18; Length 21;
Best Local Similarity 50.0%; Pred. No. 7.1e+03; Indels 0; Gaps 0;
Matches 8; Conservative 6; Mismatches 2;
Qy 2 CUGAGUTUCATUGCAGG 17
Db 18 CIGATTCCTTGTAAG 3

RESULT 36
US-10-751-736-12518
Sequence 108838, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066

RESULT 36
US-10-751-736-12518
Sequence 108838, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066

RESULT 37
US-10-719-900-134100/c
Sequence 134100, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 134100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-134100

Query Match 75.3%; Score 12.8; DB 19; Length 25;
Best Local Similarity 56.2%; Pred. No. 7.3e+03; Indels 0; Gaps 0;
Matches 9; Conservative 5; Mismatches 2;
Qy 1 CCUGAUUUCAUUGCAG 16
Db 9 CCAGATTTCATGGAG 24

RESULT 38
US-10-719-900-200558
Sequence 200558, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 200558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-200558

Query Match 75.3%; Score 12.8; DB 19; Length 25;
Best Local Similarity 56.2%; Pred. No. 7.3e+03; Indels 0; Gaps 0;
Matches 9; Conservative 5; Mismatches 2;
Qy 2 CUGAUUUCAUUGCAG 17
Db 7 CIGATTCCTTGAGG 22

```

RESULT 39
US-10-719-900-220971
; Sequence 220971, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 220971
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-220971

Query Match 75.3% Score 12.8; DB 19; Length 25;
Best Local Similarity 50.0%; Pred. No. 7, 3e+03; 6; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 5; CCGTATTAATGGCAG 20

Qy      1 CCGTATTAATGGCAG 16
Db      1||:|::|:||| 5 CCGTATTAATGGCAG 20

RESULT 40
US-10-719-900-220972
; Sequence 220972, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
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; NUMBER OF SEQ ID NOS: 982914
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-220972

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Db      1||:|::|:||| 5 CCGTATTAATGGCAG 20

Search completed: May 13, 2005, 18:25:00
Job time : 147.964 secs

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GenCore version 5.1.6
copyright (c) 1993 - 2005 Compugen Ltd.

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Total number of hits satisfying chosen parameters:	34239544 seqs, 19032134700 residues	
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AUTHORS	Caryophyllales; Amaranthaceae; Beta.							
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Heuwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,								
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.								
and Radloff, U.								
ADIS	Construction of a 'unigene' cDNA clone set by oligonucleotide							
Max-Planck-Institute for Plant Breeding Research	fingerprinting allows access to 25 000 potential sugar beet genes							
Carl-von-Linne Weg 10, 50829 Koeln, Germany								
Fax: 0049215062851								
Email: weissaar@mpiz-koeln.mpg.de								
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Max-Planck-Institute for Plant Breeding Research								
Carl-von-Linne Weg 10, 50829 Koeln, Germany								
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Carl-von-Linne Weg 10, 50829 Koeln, Germany	line)"							
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Email: weissaar@mpiz-koeln.mpg.de	/db_xref="taxon:161934"							
Insert length: 73	Std Error: 0.00							
Plate: 23	row: E	column: 15						
Seq primer: SF6; CATACTGTTAGGTGACACTATAG.								
FEATURES	Location/Qualifiers							
SOURCE	1..73							
COMMENT	/organism="Beta vulgaris"							
ADIS DNA core facility at MPIZ	/mol_type="mRNA"							
Max-Planck-Institute for Plant Breeding Research	/cultivar="KWS2320 (double haploid, monogerm breeding							
Carl-von-Linne Weg 10, 50829 Koeln, Germany	line)"							
Fax: 0049215062851	/db_xref="GABI:191784"							
Email: weissaar@mpiz-koeln.mpg.de	/db_xref="taxon:161934"							
Insert length: 73	Std Error: 0.00							
Plate: 23	row: E	column: 15						
Seq primer: SF6; CATACTGTTAGGTGACACTATAG.								
FEATURES	Location/Qualifiers							
SOURCE	1..73							
COMMENT	/organism="Beta vulgaris"							
ADIS DNA core facility at MPIZ	/mol_type="mRNA"							
Max-Planck-Institute for Plant Breeding Research	/cultivar="KWS2320 (double haploid, monogerm breeding							
Carl-von-Linne Weg 10, 50829 Koeln, Germany	line)"							
Fax: 0049215062851	/db_xref="GABI:191784"							
Email: weissaar@mpiz-koeln.mpg.de	/db_xref="taxon:161934"							
Insert length: 73	Std Error: 0.00							
Plate: 23	row: E	column: 15						
Seq primer: SF6; CATACTGTTAGGTGACACTATAG.								
FEATURES	Location/Qualifiers							
SOURCE	1..73							
COMMENT	/organism="Beta vulgaris"							
ADIS DNA core facility at MPIZ	/mol_type="mRNA"			</td				

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAGGGAGCCGCCGCTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 78.8%; Score 13.4; DB 1; Length 94;

Best Local Similarity 53.3%; Pred. No. 2.9e+04; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 5 0 CTCGCTTCATTCAG 64
| : | :: | : | : |||
polylinker; Site_1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAGGGAGCCGCCGCTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 78.8%; Score 13.4; DB 1; Length 94;

Best Local Similarity 53.3%; Pred. No. 2.9e+04; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

RESULT 6 CK098392 DEFINITION A013P34 5PR Hybrid aspen plasmid library Populus tremuloides cDNA clone A013P34 5, mRNA sequence.

ACCESSION CK098392.1 VERSION GI:30582717

KEYWORDS EST, SOURCE ORGANISM Populus tremula x Populus tremuloides

A013P34 5'PR Hybrida tremuloides mRNA linear EST 01-DEC-2003
tremuloides cDNA clone A013P34 5, mRNA sequence.
CK098392

REFERENCE 1 (bases 1 to 97)
AUTHORS Sterky, P., Blalero, R.R., Unneberg, P., Segerman, B., Nilsson, P., Brunner, A.M., Campaa, L., Jonsson-Lindwall, J., Tandre, K., Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalaria, R.P., Nilsson, O., Sandborg, G., Karlsson, J., Lundberg, J. and Jansson, S.

TITLE A Populus EST resource for functional genomics

JOURNAL Unpublished (2003)
COMMENT Other ESTs: A013P4U

Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.

FEATURES Source
Location/Qualifiers
1. .82
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BXR623"
/db_xref="txon:4558"
/clone="1116P-26"
/tissue="green leaf and root tissue"
/clone_id="pooled green leaf and root tissue"
/note="Vector: pBluescript II (SK); Site_1: EcoRI; Site_2: EcoRI"; Vector: pBluescript II (SK); Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 76.5%; Score 13; DB 2; Length 82;

Best Local Similarity 61.5%; Pred. No. 4.6e+04; Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 7 6 ATTGATTGCAAG 64
| : | :: | : | : |||
/note="Vector: pBluescript SK; Site_1: SalI; site_2: NotI; /clone=A013P34"
/tissue="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E. coli"
/clone lib="Hybrid aspen plasmid library"
/note="Vector: pBluescript SK; Site_1: SalI; site_2: NotI; Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. cDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."

ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 97;

Best Local Similarity 53.3%; Pred. No. 2.9e+04; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 5 0 CTGCTTCATTCAG 64
| : | :: | : | : |||
polylinker; Site_1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAGGGAGCCGCCGCTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 78.8%; Score 13.4; DB 1; Length 94;

Best Local Similarity 53.3%; Pred. No. 2.9e+04; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

RESULT 8 BE317163/LOCUS BE317163 DEFINITION NT0069AU5LFF1033 Developing leaf mRNA linear Medicago truncatula cDNA clone

ACCESSION BE317163 VERSION BE317163.2 GI:11961946

KEYWORDS EST

SOURCE ORGANISM Medicago truncatula (barrel medic)

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago

REFERENCE 1 (bases 1 to 52)

AUTHORS Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula Leaf Library

Unpublished (2000)

COMMENT On Jul 14, 2000 this sequence version replaced gi:9190940.

Query Match 78.8%; Score 13.4; DB 7; Length 97;

Best Local Similarity 53.3%; Pred. No. 2.9e+04; Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 2 CUGAUUCAUTGCG 16

Contact: May GD

AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geissel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thoising, B., Wyly, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE	The WASHU-HRM Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
FEATURES	This clone is available royalty-free through LILN; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI: 595027 Possible reversed clone; polyA not found.
Source	Location/Qualifiers
	1. .69 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J x DBA/2J F1" /db_xref=taxon:10090" /clone="IMAGE:1080731" /tissue_type="embryo" /dev_stage="2-cell" /lab_host="DH10B" /clonelib="Kroyles Solter mouse 2 cell" /note="Organ: embryo; Vector: pBluescribe (modified); Site 1: MuL; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13, 500 2-cell stage embryos. Primer: SalI(dN): 5'-GGTCGACCGTGACGGTTTCTTCTT-3'; CDNAS were cloned into the MuL/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1-2 kb."
ORIGIN	
Query Match	75.3%; Score 12.8; DB 1; Length 69;
Best Local Similarity	50.0%; Pred. No. 5.7e+04;
Matches	8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY	1 CCUGAUUCATUGCAG 16
Db	57 CGGTGATTTCATGGCTG 42
RESULT 12	
LOCUS	CR170276
DEFINITION	Reverse strand read from insert in 5' Hprt insertion targeting and chromosome engineering clone MHPN30d02, genomic survey sequence.
ACCESSION	CR170276
VERSION	CR170276.1
KEYWORDS	GI:49949125
SOURCE	GSS; genome survey sequence; MICER.
ORGANISM	Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.	
REFERENCE	1. (bases 1 to 71)
AUTHORS	Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Regge, J., and Bradley, A.
TITLE	Direct Submission
JOURNAL	Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK http://www.sanger.ac.uk/MICER
FEATURES	Location/Qualifiers
Source	
	1. .71 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /clone="MHPN30d02" /clone_id="MHPN"
ORIGIN	
Query Match	75.3%; Score 12.8; DB 8; Length 75;
Best Local Similarity	56.2%; Pred. No. 5.8e+04;
Matches	9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY	2 CUGAUUCATUGCAG 17
Db	62 CTAATTCATGGCTG 47
RESULT 14	
LOCUS	BB316157/C
DEFINITION	INFO29F07LF1P1059 Developing leaf Medicago truncatula cDNA clone NF029F07LF 5', rRNA sequence.

ACCESSION	BE316157	Sequencing primer: SP6	
VERSION	BE316157.2	This sequence is from a Xenopus Gene Collection (XGC) library	
KEYWORDS	EST;	constructed by Aaron M. Zorn.	
SOURCE	Medicago truncatula (barrel medic)	cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.	
ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.	ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.	
REFERENCE	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Irman, J.T., Weiler, J.W. and May, G.D.	Vector: pCS107; Site_1: EcoRI; Site_2: NotI	
AUTHORS	Expressed Sequence Tags from the Samuel Roberts Noble Foundation	Host: Escherichia coli XLI-blue.	
JOURNAL	Medicago truncatula leaf library	Location/Qualifiers	
COMMENT	Unpublished (2000)	1..85	
CONTRACT	On July 14, 2000 this sequence version replaced gi:9189934.	/organism="Xenopus tropicalis"	
PLANT_BIOLOGY	Plant Biology Division	/mol_type="mRNA"	
THE_SAMUEL_ROBERTS_NOBLE_FOUNDATION	The Samuel Roberts Noble Foundation	/db_xref="TBG005p10"	
ADDRESS	2510 Sam Noble Parkway, Ardmore, OK 73402, USA	/dev_Status="egg"	
TELEPHONE	Tel: 580 224 6650	/lab_host="Escherichia coli XLI-blue"	
FAX	Fax: 580 224 6692	/clone_lib="XGC-99"	
EMAIL	Email: gdmay@noble.org	/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"	
Medicago Genome Initiative accession: MGI:S:17512			
FEATURES			
SOURCE			
ORIGIN			
Query Match	75.3%; Score 12.8; DB 2; Length 77;	Query Match	75.3%; Score 12.8; DB 1; Length 85;
Best Local Similarity	56.2%; Pred. No. 5.8e+04;	Best Local Similarity	56.2%; Pred. No. 5.9e+04;
Matches	9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	Matches	9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY	1 CGUGAUUCAUCAGCAG 16	QY	1 CCTGAAUTCAUCAGCAG 16
Db	35 CTTGAGTCATGCCAG 20	Db	35 CCTGGTTCATGCCAG 20
RESULT	15	RESULT	16
ALB4774/C	ALB4774 mRNA linear EST 26-NOV-2003	CKL08729/c	CKL08729 mRNA linear EST 01-DEC-2003
LOCUS	85 bp mRNA clone TBgg005p10 5', mRNA	LOCUS	88 bp mRNA linear Populus tremula cDNA
DEFINITION	sequence.	DEFINITION	clone 1064P85 5', mRNA sequence.
ACCESSION	ALB4774	ACCESSION	CKL08729
VERSION	ALB4774.2	VERSION	CKL08729.1
KEYWORDS		KEYWORDS	EST.
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
ORGANISM		ORGANISM	
Populus tremula		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids I; Malpighiales; Salicaceae; Salicaceae; Populus	
1 (bases 1 to 88)		1 (bases 1 to 88)	
STERKY, P., BHALERAO, R.R., UHNEBERG, P., SEGERMAN, B., NILSSON, P., BRUNNER, A.M., CAMPAGNA, L., JONSSON, LINDBLAD, T., TANDRE, K., STRAUSS, S.H., SUNDBERG, B., GUSTAFSSON, P., UHLÉN, M., BHALERAO, R.P., NILSSON, O., SANDBERG, G., KARLSSON, J., LUNDHEDBERG, J. and JONSSON, S.			
ALB4774	XGC-egg Xenopus tropicalis EST project 2001 (11_2003)	COMMENT	Contact: Bo Seegerman
VERSION	EST.	COMMENT	Umeå Plant Science Center, Department of Plant Physiology
KEYWORDS		COMMENT	Umeå University 901 87 Umeå, Sweden
SOURCE	Xenopus tropicalis (western clawed frog)	FEATURES	901 87 Umeå, Sweden
ORGANISM	Xenopus tropicalis (western clawed frog)	source	Tel: +46 90 786 6376
Keropidae; Batrachia; Anura; Mesobatrachia; Pipidae;			Fax: +46 90 786 6376
Xenopidae; Xenopus; Silurana.			Email: bo.seegerman@plantphys.umu.se.
REFERENCE			
AUTHORS	1 (bases 1 to 85)		
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.			
TITLE	Xenopus tropicalis EST project 2001 (11_2003)		
JOURNAL	Unpublished (2003)		
COMMENT	On Sep 15, 2002 this sequence version replaced gi:22868039.		
Contact: Taylor R			
Sanger Institute			
Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: tcrp@sanger.ac.uk			
Sanger Xenopus tropicalis EST project 2001			
TROPICALIS_SEQUENCE_ID: TBgg005p10.pksp6			
ORIGIN			
Query Match	75.3%; Score 12.8; DB 7; Length 88;	Query Match	75.3%; Score 12.8; DB 7; Length 88;
Best Local Similarity	56.2%; Pred. No. 5.9e+04;	Best Local Similarity	56.2%; Pred. No. 5.9e+04;
Matches	9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	Matches	9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
Contract	Robert Strausberg, Ph.D.
Email:	cgbbsr@mail.nih.gov
Tissue Procurement	Christopher Meskaliuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation	M. Bento Soares, Ph.D.
CDNA Library Arrayed by	Greg Lennon, Ph.D.
DNA Sequencing by	Washington University Genome Sequencing Center
Clone distribution	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bi.llnl.gov/bbcp/image/image.html
FEATURES	Trace considered overall poor quality
Source	Insert Length: 1052 Std Error: 0.00
Seq primer:	-40m13 fwd. Et from Amersham High quality sequence Btop: 1.
Location/Qualifiers	Location/Qualifiers
	1. .40
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:1560223"
	/tissue_type="adenocarcinoma"
	/lab_host="DHBLB"
	/clone_lib="NCI CGAP_Co8"
	/note="Organ: Colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo (dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN	Query Match
	Best Local Similarity 72.9%; Score 12.4; DB 1; Length 40;
	Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy	1 CCUGAUUCAUUGC 14
Db	40 CCTGATTAAATTC 27
RESULT 20	Query Match
BZ594604/c	Score 12.4; DB 8; Length 50;
LOCUS	Best Local Similarity 57.1%; Pred. No. 8. 9e+04;
DEFINITION	Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
ACCESSION	AAV60149
VERSION	AAV60149.1
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 54)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geissel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HMM Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project
WASHU-HMM Mouse EST Project	Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
Tel: 314 866 1800	
Fax: 314 286 1810	
Email: mouseest@watson.wustl.edu	
FEATURES	This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
source	MGU65333
Seq primer:	-28m13 rev1 ET from Amersham.
Location/Qualifiers	Location/Qualifiers
	1. .54
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="C57BL/6"
	/db_xref="taxon:10090"
	/clone="IMAGE:1227741"
	/sex="females"
	/tissue_type="whole skin"
	/dev_stage="11 weeks old"
	/lab_host="SOIR (Kanamycin resistant)"
	/clone_lib="Stratagene mouse skin (#937313)"
	/note="Organ: Skin; Vector: pBluscript SK-; Site1: EcoRI; Site2: XbaI; Cloned unidirectionally. Primer:
COMMENT	Contract: Joseph R. Ecker
	Salk Institute Genomic Analysis Laboratory (SIGnAL)
	The Salk Institute for Biological Studies
	1000 N. Torrey Pines Road, La Jolla, CA 92037, USA
	Tel: 858 453 4100 ext 1752
	Fax: 858 559 6379
	Email: ecker@salk.edu

Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR vector; -5' adaptor sequence: 5' CTGAGTTTTTTTTTTT 3'."

ORIGIN

Query Match 72.9%; Score 12.4; DB 1; Length 54;
 Best Local Similarity 64.3%; Pred. No. 9⁺⁰⁴;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GUUNUCAUGCGG 17
 Db 38 GATTCATGGCAGG 51

Query Match 72.9%; Score 12.4; DB 8; Length 61;
 Best Local Similarity 50.0%; Pred. No. 9.2⁺⁰⁴;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCUGAUUTCAUGC 14
 Db 17 CCTGATTTAATGC 30

RESULT 22
 AZ762535 LOCUS AZ762535 DEFINITION IM0557G06R Mouse 10kb plasmid UGCGLM library Mus musculus genomic clone UGCGLM0557G06 R, genomic survey sequence.
 ACCESSION AZ762535 VERSION AZ762535.1 GI:12872637
 KEYWORDS GSS SOURCE
 ORGANISM Mus musculus (house mouse)
 Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 61)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tunney, A., von Niederauhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: bweiss@utah.edu
 Invert. length: 10000 Std Error: 0.00
 Plate: 0557 Row: G Column: 06
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: Plasmid ends
 High quality sequence, stop: 61.

LOCATION/QUALIFIERS
 FEATURES source
 ORIGIN

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10909"
 /clone="UGCGLM0557G06"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lip="Mouse 10kb plasmid UGCGLM library from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www-jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 61;
 Best Local Similarity 50.0%; Pred. No. 9.2⁺⁰⁴;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCUGAUUTCAUGC 14
 Db 17 CCTGATTTAATGC 30

RESULT 23
 CL528748/C LOCUS CL528748 DEFINITION ASV7F11.fwd ASLV-vector integration sites in human 293T-TVA cells clone UGCGLM0557G06 genomic clone ASV7F11.fwd, genomic survey sequence.
 ACCESSION CL528748 VERSION CL528748.1 GI:47421959
 KEYWORDS GSS SOURCE
 ORGANISM Homo sapiens
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. REFERENCE 1 (bases 1 to 61)
 AUTHORS Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shiu, P., Chen, H., Berry, C.C., Ecker, J.R. and Bushman, F.
 TITLE Retroviral DNA Integration: ASLV, HTV and MLV Show Distinct Target Site Preferences
 JOURNAL Unpublished (2004)
 COMMENT Contact: Frederic Bushman
 The Salk Institute for Biological Studies
 10010 N. Torrey Pine Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1630
 Fax: 858 554 0341
 Email: bushman@salk.edu
 Class: PCR with specific primers.
 LOCATION/QUALIFIERS
 FEATURES source
 ORIGIN

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="ASV7F11.fwd"
 /clone_lip="ASLV-vector integration sites in human 293T-TVA cells"
 /note="Human 293T cells expressing the subgroup A avian retrovirus receptor (293T-TVA) were infected with an ASLV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNA was amplified using one primer that bound to the linker DNA and one that bound to the ASLV proviruses and cellular DNA were cloned and sequenced."
 Query Match 72.9%; Score 12.4; DB 9; Length 61;
 Best Local Similarity 57.1%; Pred. No. 9.2⁺⁰⁴;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 CUGAUUCAUUGCA 15
 Db 38 CTGACTCTATGCA 25

RESULT 24
 BH866175/C LOCUS BH866175
 DEFINITION SALK_100839 Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK_100839, genomic survey sequence.

ACCESSION	BH86175	TITLE	Weisshaar, B.	
VERSION	BH86175.1	JOURNAL	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics	
KEYWORDS	GSS.	PUBLISHED	Plant Mol. Biol. 53 (1-2), 247-259 (2003)	
SOURCE	Arabidopsis thaliana (thale cress)	REFERENCE	2311747	
ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis	AUTHORS	1475621	
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome	JOURNAL	Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.	
JOURNAL	Unpublished (2001)	PUBLISHED	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines	
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu	REFERENCE	Biotechniques 35 (6), 1164-1168 (2003)	
TDNA	This is single pass sequence recovered from the left border of TDNA.	COMMENT	3	
Class:	TDNA tagged.	TDNA	TDNA	
FEATURES	Location/Qualifiers	LOCATION	2304198	
Source	1..63	PUBLISHED	14682050	
Query Match	72.9%; Score 12.4; DB 8; Length 63;	REFERENCE	4 (bases 1 to 65)	
Best: Local Similarity 50.0%; Pred. No. 9.2e+04; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	/organisms="Arabidopsis thaliana" 'mol_type="genomic DNA" 'ecotype="Col-0" 'db_xref="taxon:3702" 'clone_lid="SALK_108393" 'clone_lid="Arabidopsis thaliana TDNA insertion lines" 'notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html "	AUTHORS	Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.	
ORIGIN		JOURNAL	Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50029, Germany	
RESULT	25	COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g51880. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpz-koeln.mpg.de/GABI-Kat/ .	
LOCUS	CR769564	FEATURES	1..65	
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-032E03-027723, genomic survey sequence.	Source	/organism="Arabidopsis thaliana" 'mol_type="genomic DNA" 'strain="Columbia 0" 'db_xref="taxon:3702"	
ACCESSION	CR769564	Query Match	72.9%; Score 12.4; DB 9; Length 65;	
VERSION	CR769564.1	Best Local Similarity 50.0%; Pred. No. 9.3e+04; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	Query	2 CUGAUUCAUAGCA 15
KEYWORDS	GSS	Db	1.. ::: :: ::	
SOURCE	Arabidopsis thaliana (thale cress)	Result	52 CGATTCCTTGCA 39	
ORGANISM	Arabidopsis thaliana	RESULT	26	
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis	ACCESSION	CG606249	
AUTHORS	Li, Y., Rosso,M.G., Strizhov,N., Vrehoever,P. and Weishaar,B.	LOCUS	CG606249	
TITLE	GAB-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana.	DEFINITION	OSTR83929 Mus musculus 129sv/Ev Mus musculus cDNA clone OSTR83929, mRNA sequence.	
REFERENCE	1	ACCESSION	CG606249	
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)	VERSION	CG606249.1	
MEDLINE	22755829	KEYWORDS	GI:37429925	
PUBMED	12874060	ORGANISM	Mus musculus (house mouse)	
REFERENCE	2	SOURCE	GSS	
AUTHORS	Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and	REFERENCE	1 (bases 1 to 65)	
REFERENCE	Zambrowicz,B.P., Abun,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., Beltran-del Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Kipp,P., Kohlhauff,B., Ma,Z.-O., Makejeich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,	AUTHORS	Zambrowicz,B.P., Abun,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., Beltran-del Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Kipp,P., Kohlhauff,B., Ma,Z.-O., Makejeich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,	

TITLE	Zhu, Q., Person, C. and Sands,A.T. Whirl kinase deficiency lowers blood pressure in mice: a gene-trap
JOURNAL	4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@exgen.com
COMMENT	Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
FEATURES	Class: Gene Trap Location/Qualifiers
Source	1. .65 'organism="Mus musculus" 'mol_type="mRNA" 'strain="129S/Ev" 'db_xref="taxon:10090" 'clone_xref="EST283929" 'cell_type="embryonic stem cell" 'clone_lib="Mus musculus 129Sv/Ev"
ORIGIN	Query Match 72.9%; Score 12.4; DB 9; Length 65; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY	3 ugauuucauugca 16
Db	8 TGTATTCACTGCGAG 21
RESULT	27
ACCESSION	AL853876
DEFINITION	XGC-egg Xenopus tropicalis mRNA clone TEG9005021 3', mRNA sequence.
VERSION	AL853876.2
KEYWORDS	EST.
SOURCE	Parastromyloides trichosuri
ORGANISM	Parastromyloides trichosuri
REFERENCE	1 (bases 1 to 74) Panagrolaimoidea: Strongyloidae; Parastromyloides
AUTHORS	McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Danté, M., Marra, M., Hillier, L., Kucaba, T., Thising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Traagardishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, A., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
TITLE	EST.
JOURNAL	The Washington Univ. Nematode EST Project, 1999 Unpubl shd (1999)
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
REFERENCE	1 (bases 1 to 67) Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
AUTHORS	Sanger Xenopus tropicalis EST project 2001 (11_2003)
TITLE	Unpublished (2003)
JOURNAL	On Sep 15, 2002 this sequence version replaced g1:22874096.
COMMENT	Contact: Taylor R Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk
FEATURES	Sanger Xenopus tropicalis EST project 2001
Source	TROPICALIS SEQID: TEG9005021.qikT7 Sequencing primer: T7
QY	This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Db	Vector: pCS107; Site_1: ECORI; Site_2: NotI Host: Escherichia coli XL1-blue.
FEATURES	Location/Qualifiers
Source	1. .74 'organism="Xenopus tropicalis" 'mol_type="mRNA" 'db_xref="taxon:8364" 'clone_xref="TEG9005021" 'dev_stage="parasitic" 'lab_host="PCR10B" 'clone_lib="Parastromyloides trichosuri PA SL1 TOPO v1 Murphy Chiapelli McCarter" 'note="Vector: PCR1-TOPO (Invitrogen); Site_1: ECORI; The library was constructed by Claire Murphy, Brandi Chiapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo (dT)-SL1 PCR based library. Parastromyloides trichosuri parasitic adult cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dt) on the 3' end were non-directionally cloned into PCR1-TOPO(Invitrogen) following the TOPO TA cloning protocol. Nematodes were provided by Dr. Warwick Grant of AgResearch, New Zealand. Worms were harvested from Australian brush-tailed possum (Trichosurus vulpecula)

and washed thoroughly to remove host contamination. Note that despite this effort, host contamination of the library is possible."

ORIGIN

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	2	CUGAUUCAUNGCA 15	50.0%	9.4e+04	74	0	1	0
Db	25	CTGATTTCATTCGA 12	50.0%	9.4e+04	74	0	1	0

RESULT 29

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	2	CUGAUUCAUNGCA 15	50.0%	9.4e+04	74	0	1	0
Db	25	CTGATTTCATTCGA 12	50.0%	9.4e+04	74	0	1	0

RESULT 29
A2468373/c
LOCUS 1M0281A2ZP Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UNGCIM0281A2Z P, genomic survey sequence.

DEFINITION

ACCESSION A2468373

VERSION A2468373.1

KEYWORDS

GSS: Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 74)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0281 row: A column: 22

Seq primer: CCTGTGAAACACGGCCAGT

Class: Plasmid ends

High quality sequence stop: 74.

Location/Qualifiers

1. .?4

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10990"

/clone="UNGCI0281A2Z"

/sex="Male"

/lab_host="E. Coli Strain XL10-Gold, Ti-resistant, F-

/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PWD2Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (pGI473211|gb|AF129072.1), a copy-number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

ORIGIN

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	1	CCGUAUCAUNGCA 14	50.0%	9.4e+04	74	0	1	0
Db	23	CCGTGATTTCATTCGA 10	50.0%	9.4e+04	74	0	1	0

RESULT 30

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	1	CCGUAUCAUNGCA 14	50.0%	9.4e+04	74	0	1	0
Db	23	CCGTGATTTCATTCGA 10	50.0%	9.4e+04	74	0	1	0

RESULT 30
B2593321
LOCUS B2593321 Arabidopsis thaliana genomic clone SALK_070016.16.25.x, genomic survey sequence.

DEFINITION

B2593321

VERSION B2593321.1

KEYWORDS

GSS:

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 77)

AUTHORS

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shim, P., Zimmerman, J. and Becker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Becker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 585 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .?77

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_070016.16.25.x"

/clone_id="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	2	CUGAUUCAUNGCA 15	50.0%	9.4e+04	77	0	1	0
Db	57	CTGATTTCATTCGA 70	50.0%	9.4e+04	77	0	1	0

RESULT 31

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gap
Qy	1	CCGUAUCAUNGCA 14	50.0%	9.4e+04	77	0	1	0
Db	23	CCGTGATTTCATTCGA 10	50.0%	9.4e+04	77	0	1	0

RESULT 31
AW672652/c
LOCUS AW672652 mRNA linear EST 26-SEP-2001

ORIGIN

adaptored vector DNA, and transformed into chemically-competent E. coli XL1-Gold (Stratagene) cells and selected for ampicillin resistance."

	DEFINITION	ORGANISM
REFERENCE	1x Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo. <i>Rattus norvegicus</i> cDNA similar to or similar to: gb U05091.1 MMU65091 Mus musculus megalocyte-specific gene 1 (msg1) mRNA, mRNA sequence.	Glycine max
ACCESSION	AW672652	Bivalvia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
VERSION	AW672652.1	1 (bases 1 to 80)
KEYWORDS	EST.	Shoemaker, R.; Keim, P.; Vodkin, L.; Erpelding, J.; Coryell, V.; Khanna, A.; Bolla, B.; Marra, M.; Hillier, L.; Kubota, T.; Martin, J.; Beck, C.; Wyly, T.; Underwood, K.; Steptoe, M.; Theising, B.; Allen, M.; Bowers, Y.; Person, B.; Swaller, T.; Gibbons, M.; Pape, D.; Harvey, N.; Schurk, R.; Ritter, E.; Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.; Waterston, R.; and Wilson, R.
AUTHORS	Rattus norvegicus (Norway rat)	Public Soybean EST Project
TITLE	Rattus norvegicus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	Unpublished (1999)
JOURNAL	Kidney: gene expression study by differential display Genesis 27 (1), 22-31 (2000)	Contact: Shoemaker R/Public Soybean EST Project
MEDLINE	20021327	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
PUBMED	108662152	Tel: 314 286 1800 Fax: 314 286 1110
COMMENT	Contact: Plisov S.Y. Laboratory of Comparative Carcinogenesis National Cancer Institute NCI, Bldg. 35B, Room 205, Frederick, MD 21702, USA Tel: 301 846 1242 Fax: 301 846 4956 Email: Plisov@mail.ncifcrf.gov	Email: est@watson.wustl.edu
PCR PRIMERS		When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Putative full length read vector to vector length is 81 Seq primer: -40RP from Gibco.
FORWARD:	ctcgaggccatgtac	Location/Qualifiers
BACKWARD:	ttaaggttttttttta	1..80
SEQUENCE LENGTH:	79	/organism="Glycine max"
SEQUENCE SOURCE	Std Error: 0.00	/mol_type="mRNA"
FEATURES		/db_xref="taxon:10116"
FEATURES SOURCE		/tissue_type="Metanephric mesenchyme"
FEATURES SOURCE		/cell_type="Mesenchymal/Epithelial"
FEATURES SOURCE		/dev_stge="13 dpb-16dpb"
FEATURES SOURCE		/lab_host="JMI09"
FEATURES SOURCE		/clone_lib="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."
FEATURES SOURCE		/note="Organ: Kidney; Vector: pGEM-Teasy (Promega); Restriction Enzymes: 1; AvrI, AattII, SphI, NcoI, BstZRI, NotI, SacII, and EcoRI Spel, EcoRI, NotI, BstZRI, PstI, SalI, NdeI, SacII, BstXII, and NsiI cDNA fragment, PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."
ORIGIN		
Query Match	72.9%; Score 12.4; DB 2; Length 79;	
Best Local Similarity	57.1%; Pred. No. 9.5e+04; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	
Qy	3 UGAUTTCACTGGAG 16	
Db	35 TAATTTCAGTGCGAG 22	
RESULT	32	
BUS25856	BUS25856	Query Match 72.9%; Score 12.4; DB 5; Length 80;
DEFINITION	BB8810-Y1 Gm-c1036 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1036-10771 5', mRNA sequence.	Best Local Similarity 50.0%; Pred. No. 9.6e+04; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
ACCESSION	BUS25856	
VERSION	BUS25856.1	
KEYWORDS	EST.	
SOURCE	Glycine max (soybean)	
RESULT	33	
AZ339200	AZ339200	Query Match 72.9%; Score 12.4; DB 5; Length 80;
LOCUS	AZ339200	Best Local Similarity 50.0%; Pred. No. 9.6e+04; Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
DEFINITION	AM0707M06R Mouse 10kb plasmid UGCGM library Mus musculus genomic DNA sequence.	
ACCESSION	AZ339200	
VERSION	AZ339200.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	

Euksaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 81)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meinen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhäusern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0070 row: M column: 06
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 81.
Location/Qualifiers

FEATURES
Source

1. .81
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGCIM0070006"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UniCCM library"
 /note="Vector: PWP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.Jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWP42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid pL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
competent vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 81;
Best Local Similarity 50.0%; Pred. No. 9.6e+04; Matches 7; Conservatve 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGC 14
 Db 57 CCTGGTTTCATGCC 44

FEATURES
Source

1. .82
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/KS5"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3590 - RescueMu Grid M"
 /note="Organ: Leaf; Vector: RescueMu (engineered from
BlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site: www.zmud.iastate.edu, and follow the links for
RescueMu." Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 82;
Best Local Similarity 50.0%; Pred. No. 9.6e+04; Matches 7; Conservatve 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUUCAUUGC 14
 Db 57 CCTGGTTTCATGCC 44

RESULT 35
 CN855612/c
 LOCUS CN855612
 DEFINITION 00721AAA002849RT (AAAA) Royal Gala 59 DfFB fruit, seeds removed
 Malus x domestica cDNA clone AA002849, mRNA sequence.
 ACCESSION CN855612
 VERSION CN855612.1 GI:48110989
 KEYWORDS EST
 SOURCE
 ORGANISM Malus x domestica (cultivated apple)

Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 roids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 1 (bases 1 to 83)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Martinez, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
 B2587139 Unpublished (2004)
 Contact: Gleave, A.
 Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Ltd
 Zea maya
 ORGANISM Zea maya

Query Match		72.9%	Score 12.4;	DB 8;	Length 83;
Best Local Similarity		57.1%	Pred. No. 9.6e+04;		
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Arabidopsis	thaliana	clone UUGC2M092P06 R,	genomic survey sequence.		
BH791384		16			
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GSS					
BH791384..1	GI:19885192				
Arabidopsis thaliana	(thale cress)				
Arabidopsis	thaliana				
Eukaryota;	Viridiplante;	Stereophyta;	Embryophyta;	Tracheophyta;	
Spermatophyta;	Magnoliophyt;	eudicotyledons;	core eudicots;		
rosids;	euroids II;	Brassicales;	Brassicaceae;	Arabidopsis.	
1	(bases 1 to 83)				
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Prednis,L.,					
Gadrinar,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,					
Shinn,P., Zimmerman,J. and Ecker,J.R.					
A Sequence-Indexed Library of Insertion Mutations in the					
Arabidopsis Genome					
Unpublished (2001)					
Contact: Joseph R. Ecker					
Salk Institute Genomic Analysis Laboratory (SIGnAL)					
The Salk Institute for Biological Studies					
1001 N. Torrey Pine Road, La Jolla, CA 92037, USA					
Tel: 858 453 4100 x1752					
Fax: 858 6379					
Email: ecker@salk.edu					
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g44580.					
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Location/Qualifiers					
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Arabidopsis	thaliana	clone UUGC2M092P06 R,	genomic survey sequence.		
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GSS					
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Arabidopsis	thaliana				
Eukaryota;	Viridiplante;	Stereophyta;	Embryophyta;	Tracheophyta;	
Spermatophyta;	Magnoliophyt;	eudicotyledons;	core eudicots;		
rosids;	euroids II;	Brassicales;	Brassicaceae;	Arabidopsis.	
1	(bases 1 to 83)				
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Gadrinar,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,					
Shinn,P., Zimmerman,J. and Ecker,J.R.					
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Arabidopsis Genome					
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Fax: 858 6379					
Email: ecker@salk.edu					
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Class: TDNA tagged.					
Location/Qualifiers					
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SALK_059855..54.50.x	Arabidopsis thaliana genomic clone	91 bp	linearity GSS 20-FEB-2001		
Arabidopsis	thaliana	clone UUGC2M092P06 R,	genomic survey sequence.		
BH791384		16			
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GSS					
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rosids;	euroids II;	Brassicales;	Brassicaceae;	Arabidopsis.	
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Gadrinar,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,					
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ch		72.9%	Score 12.4; DB 7; length 83;		
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Arabidopsis	thaliana	clone UUGC2M092P06 R,	genomic survey sequence.		
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SALK_059855..54.50.x	Arabidopsis thaliana genomic clone	91 bp	linearity GSS 20-FEB-2001		
Arabidopsis	thaliana	clone UUGC2M092P06 R,	genomic survey sequence.		
BH791384		16			
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Query Match	72.9%	Score 12.4; DB 8;	Length 91;
Best Local Similarity	57.1%	Pred. No. 9.7e+04;	
Matches	8;	Conservative	
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(K.Okubo)		Homo sapiens cDNA, mRNA	
REFERENCE			
CONTACT			
VERSION			
TITLE			
KEYWORDS			
EST:			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Okubo, K.			
BodyMap; human gene expression database			
Unpublished (1995)			
Contact: Okubo, K.			
Institute for Molecular and Cellular Biol			
Osaka University			
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan			
Tel: 06-877-5111(ex.3315)			
Email: kousaku@imcb.osaka-u.ac.jp			
We are not submitting the same cDNA sequence redundantly to DBJ			
since 1993. For the abundance information of clones with this			
sequence in this library and as well as in other 3'-directed			
libraries, see http://www.imcb.osaka-u.ac.jp/bodymap/ . The			
sequences of the clones represented by this GS sequences is also			
found there.			
FEATURES			
source			
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VERSION			
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SOURCE			

clone distribution: MGC clone distribution information can be

<http://image.llnl.gov>
Plate: LIAW1107 row: c column: 21
High quality sequence stop: 98.
Location/Qualifiers

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OKIGIN

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Query Match          72.9%;  Score 12.4;  DB 4;  Length 98;
Best Local Similarity 50.0%; Pred. No. 9.9e+04;  Mismatches 1;
Matches 7; Conservative 6; Indels 0; Gaps 0;
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 1 ccUGAUUCAUUC 14
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Search completed: May 13, 2005, 17:50:53
Job time : 845.127 secs

GenCore version 5.1.6
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OM nucleic - nucleic Search, using sw model				
Run on:	May 13, 2005, 16:49:04 ; Search time 1090.95 Seconds (without alignments)			
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Gapext	1.0			
Searched:	4708233 seqs, 24227607955 residues			
Total number of hits satisfying chosen parameters:	2238514			
Minimum DB seq length:	0			
Maximum DB seq length:	100			
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	Listing first 100 summaries			
Result No.	Score	Query Length	DB ID	Description
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2	36	94.7	37	AX583594 Sequence
3	31.8	83.7	38	AX218695 Sequence
4	31.4	82.6	38	AX218894 Sequence
5	31.4	82.6	38	AX223385 Sequence
6	31.4	82.6	38	AX580466 Sequence
7	31.2	82.1	38	AR331496 Sequence
8	30.8	81.1	38	AR331983 Sequence
9	30.8	81.1	38	AR330070 Sequence
10	30.8	81.1	38	AR331271 Sequence
11	30.6	80.5	38	AR332172 Sequence
12	30.4	80.0	38	AR332011 Sequence
13	30.4	80.0	38	AR333161 Sequence
14	30.4	80.0	38	AX219845 Sequence
15	30.4	80.0	38	AX219642 Sequence
16	30.4	80.0	38	AX222387 Sequence
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ACCESSION AX580494 VERSION AX580494.1 GI:27649696
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 2332 14-FEB-2002;
Thompson, James (US)
FEATURES SOURCE Location/Qualifiers
1. .38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:3230"
/note="Enzymatic Nucleic Acid"

ORIGIN
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Matches 31; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AX583594 VERSION AX583594.1 GI:27655404
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
JOURNAL Patent: WO 0211674-A 5432 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES SOURCE Location/Qualifiers
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match Best Local Similarity 83.7%; Pred. No. 0.0087; Length 38;
Matches 26; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

RESULT 2
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ACCESSION AX583594 VERSION AX583594.1 GI:27655404
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
JOURNAL Patent: WO 0211674-A 5432 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES SOURCE Location/Qualifiers
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ALIGMENTS

RESULT 1
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ACCESSION AX580494 VERSION AX580494.1 GI:27649696
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 2332 14-FEB-2002;
Thompson, James (US)
FEATURES SOURCE Location/Qualifiers
1. .38
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/note="Enzymatic Nucleic Acid"

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Matches 29; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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AX218695 LOCUS AX218695 DEFINITION Sequence 4137 from Patent WO0199103.
ACCESSION AX218695 VERSION AX218695.1 GI:15546419
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Blatt,L., Mcswiggen,J. and Chowriya,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 4137 16-Aug-2001; Blatt, Lawrence (US) ;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Mcswiggen, James (US) ; Chowriya, Bharat M. (US)
FEATURES SOURCE Location/Qualifiers
1. .38
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/mol_type="unassigned RNA"
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/note="Nucleic Acid"

ORIGIN
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Matches 26; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
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ACCESSION AX218894 VERSION AX218894.1 GI:15546518
KEYWORDS .
ORGANISM SOURCE synthetic construct
REFERENCE 1. other sequences; artificial sequences.
AUTHORS Blatt,L., Mcswiggen,J. and Chowriya,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

source

JOURNAL no go gene expression
Patient: WO 0159103-A 4336 16-AUG-2001; Lawrence (US) ;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowira, Bharat M. (US)
Location/Qualifiers

REFERENCE

ORIGIN

Query Match 82.6%; Score 31.4; DB 6; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 27; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db /organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

RESULT 5

DEFINITION Sequence 954 from Patent WO0162911.

ACCESSION AX273385

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.

AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and Ellis,J.H.

TITLE Method and reagent for the inhibition of grid

JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES Location/Qualifiers

Db 1. .38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 82.6%; Score 31.4; DB 6; Length 38;
Best Local Similarity 78.8%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 26; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db /organism="synthetic construct"
/mol_type="unassigned RNA"
/note="Enzymatic Nucleic Acid"

RESULT 6

LOCUS AX580466

DEFINITION Sequence 2304 from Patent WO021674.

ACCESSION AX580466

KEYWORDS .

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowiak,D.E., and Grube,A.

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)

JOURNAL Patent: WO 0311674-A 2304 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US) ;

FEATURES Location/Qualifiers

Db /organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN

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Matches 25; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db /organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

RESULT 7

DEFINITION Sequence 8898 from patent US 6566127.

ACCESSION AR331496

VERSION AR331496.1

KEYWORDS Unknown.

SOURCE ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 8898 20-MAY-2003; Location/Qualifiers

FEATURES

Db 1. .38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN

Query Match 82.1%; Score 31.2; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.016; Indels 0; Gaps 0;
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/mol_type="unassigned RNA"

RESULT 8

LOCUS AR331983

DEFINITION Sequence 9385 from patent US 6566127.

ACCESSION AR331983

VERSION AR331983.1

KEYWORDS Unknown.

SOURCE ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 9385 20-MAY-2003; Location/Qualifiers

FEATURES

Db 1. .38
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ORIGIN

Query Match 82.1%; Score 31.2; DB 6; Length 38;
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Db /organism="unknown"
/mol_type="unassigned RNA"

Db	1 CCCGCAACTGTGAGGCCGTTAGGCCGAAGTCA	36	REFERENCE 1 (bases 1 to 38) AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
RESULT 9			JOURNAL Patent: US 656127-A 9574 20-MAY-2003; Location/Qualifiers
AR330070	AR330070	38 bp RNA	DEFINITION Sequence 7472 from patent US 656127.
LOCUS			ACCESSION AR330070
VERSION			AR330070.1 GI:33715878
KEYWORDS			SOURCE Unknown.
ORGANISM			Unclassified.
REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
TITLE			JOURNAL Patent: US 656127-A 7472 20-MAY-2003; Location/Qualifiers
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ORGANISM			Unclassified.
REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
TITLE			JOURNAL Patent: US 656127-A 9413 20-MAY-2003; Location/Qualifiers
FEATURES source			1. .38 /organism="unknown" /mol_type="unassigned RNA"
ORIGIN			/mol_type="unassigned RNA"
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ORGANISM			Unknown.
REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
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KEYWORDS			Db 1 CCTCGAGCTGTGAGAAGCCGTTAGGCCGAAGAAC 32
ORGANISM			Unclassified.
REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
TITLE			JOURNAL Patent: US 656127-A 9413 20-MAY-2003; Location/Qualifiers
FEATURES source			1. .38 /organism="unknown" /mol_type="unassigned RNA"
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ORGANISM			Unclassified.
REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
TITLE			JOURNAL Patent: US 656127-A 10563 20-MAY-2003; Location/Qualifiers
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REFERENCE 1 (bases 1 to 38)			AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
AUTHORS			TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
TITLE			JOURNAL Patent: US 656127-A 10563 20-MAY-2003; Location/Qualifiers
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ACCESSION	AX218945								VERSION	AX22387.1		
VERSION	AX218945.1	GT:15546669							KEYWORDS			
KEYWORDS									SOURCE			
SOURCE									ORGANISM			
ORGANISM									Synthetic construct			
REFERENCE									other sequences; artificial sequences.			
AUTHORS									REFERENCE			
TITLE									AUTHORS			
JOURNAL									TITLE			
FEATURES									JOURNAL			
Source									Method and reagent for the modulation and diagnosis of cd20 and			
ORIGIN									noco gene expression			
Query Match	Best Local Similarity 80.0%; Score 30.4; DB 6; Length 38;								Patent: WO 0159103-A 4387 16-AUG-2001;			
Best Local Similarity 81.2%; Pred. No. 0 036; Mismatches 1; Indels 0; Gaps 0;								RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;				
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;								McSwiggen, James (US) ; Chowkira, Bharat M. (US)				
Qy	5	CAUAUCGAGGCCGUTAGCCGAAAUCA	36					FEATURES				
Db	5	: : : : : :	36					source				
RESULT 15								ORIGIN				
AX219642	AX219642	38 bp	RNA	1	linear	PAT	07-SEP-2001	Query Match	Best Local Similarity 80.0%; Score 30.4; DB 6; Length 38;			
LOCUS	Sequence 5084 from Patent WO0159103.							Matches 25; Conservative 6; Mismatches 1; Indels 0; Gaps 0;				
DEFINITION								Qy	5	CAUAUCGAGGCCGUTAGCCGAAAUCA	36	
ACCESSION	AX219642							Db	5	CAUCTCTAGGCCGTTAGCCGAAATTC	36	
VERSION	AX219642.1	GT:15547366						RESULT 17				
KEYWORDS								AR330741	AR330741	38 bp	RNA	
SOURCE								LOCUS	Sequence 8143 from patent US 6566127.		linear	
ORGANISM								DEFINITION			PAT 17-AUG-2003	
SYNTHETIC CONSTRUCT								ACCESSION	AR330741			
OTHER SEQUENCES								VERSION	AR330741.1			
REFERENCE								KEYWORDS				
AUTHORS								SOURCE				
TITLE								ORGANISM	Unknown.			
JOURNAL								REFERENCE				
FEATURES								AUTHORS				
Source								TITLE				
ORIGIN								JOURNAL				
Query Match	Best Local Similarity 78.1%; Pred. No. 0 036; Mismatches 1; Indels 0; Gaps 0;							FEATURES				
Best Local Similarity 79.5%; Score 30.2; DB 6; Length 38;								source				
Matches 25; Conservative 7; Mismatches 3; Indels 0; Gaps 0;								ORIGIN				
Qy	2	CUGCAAUUCGAGGCCGUTAGCCGAAATTC	36					Query Match	Best Local Similarity 71.4%; Pred. No. 0 044; Mismatches 3; Indels 0; Gaps 0;			
Db	2	CTACAGCTTGAGGCCGTTAGCCGAAATTC	36					Matches 25; Conservative 7; Mismatches 3; Indels 0; Gaps 0;				
FEATURES								Qy	2	CUGCAAUUCGAGGCCGUTAGCCGAAATTC	34	
Source								Db	2	CTACAGCTTGAGGCCGTTAGCCGAAATTC	34	
modified_base								RESULT 18				
ORIGIN								LOCUS	AX219074			
Query Match	BEST LOCAL SIMILARITY 75.8%; PRED. NO. 0 036; MISMATCHES 25; CONSERVATIVE 6; MISMATCHES 2; INDELS 0; GAPS 0;							DEFINITION	Sequence 4516 from Patent WO0159103.			
Qy	2	CUGCAAUUCGAGGCCGUTAGCCGAAATTC	34					ACCESSION	AX219074			

VERSION	JOURNAL	PATENT	Patent: US 6566127-A 7766 20-MAY-2003;	LOCATION/QUALIFIERS
KEYWORD SOURCE				1. .38 /organism="unknown" /mol_type="unassigned RNA"
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
2 CUGCAUCAUGAAGGAGCCGUAGGCCGAAAUCA 36				
Db				
2 CTGCAACCTGATGAGGCCGTAGGCCGAAAGTAA 36				
RESULT 21				
AR332137				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 GCGAUCGAUGAGGCCGUAGGCCGAAAUCAAGG 38				
Db				
1 CCTAAATTCTGATGAGGCCGTAGGCCGAAATTCAGG 38				
RESULT 22				
AR227896				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 (bases 1 to 38)				
RESULT 23				
AR333364				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
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ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 (bases 1 to 38)				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 24				
AR330124				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 (bases 1 to 38)				
RESULTS 25				
AR330125				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 26				
AR330126				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
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Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 27				
AR330127				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
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JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
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Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 28				
AR330128				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
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ORIGIN				
Query Match				
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Matches				
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1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 29				
AR330129				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
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Query Match				
Best Local Similarity				
Matches				
Qy				
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Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 30				
AR330130				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 31				
AR330131				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 32				
AR330132				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
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ORIGIN				
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Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 33				
AR330133				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 34				
AR330134				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 35				
AR330135				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
AUTHORS				
TITLE				
VERSION				
JOURNAL				
FEATURES				
SOURCE				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Qy				
1 .38				
Db				
1 Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor patent: US 6566127-A 20-MAY-2003;				
RESULTS 36				
AR330136				
LOCUS				
DEFINITION				
SEQUENCE				
VERSION				

RESULT 23	AX580822	AY580822	38 bp	RNA	linear	PAT 10-JAN-2003	
LOCUS			Sequence 2660 from Patent WO0211674.				
DEFINITION							
ACCESSION			AX580822				
VERSION			AX580822.1	GI:27550024			
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE	1	ccouggcaaucuauagggccgggttggccggaaauacagg	38				
AUTHORS	Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.						
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1) 2660 14-FEB-2002;						
JOURNAL	RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US); Thompson, James (US)						
FEATURES	/source						
	1..38						
	/organism="synthetic construct"						
	/mol_type="unassigned RNA"						
	/db_xref="taxon:32630"						
	/note="Enzymatic Nucleic Acid"						
ORIGIN							
Query Match	78.9%	Score 30; DB 6; Length 38;					
Best Local Similarity	83.3%	Pred. No. 0.053;					
Matches	25;	Conservative 5; Mismatches 0; Indels 0; Gaps 0;					
Qy	4	GCAAAUCUGAAGGGCGUAGGCCGAAAAA 33					
Db	4	GCAATCTGATGAGGCCGTTAGGCCGAAAAA 33					
RESULT 24	AR330838	AR330838	38 bp	RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 8240 from patent US 6566127.						
VERSION	AR330838	AR330838.1	GI:33716646				
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE	1	unclassified.					
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.						
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor						
JOURNAL	PATENT: US 6566127-A 8240 20-MAY-2003; Location/Qualifiers						
FEATURES	/source						
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	/organism="unknown"						
	/mol_type="unassigned RNA"						
ORIGIN							
Query Match	78.4%	Score 29.8; DB 6; Length 38;					
Best Local Similarity	75.8%	Pred. No. 0.065; 2; Indels 0; Gaps 0;					
Matches	25;	Conservative 6; Mismatches 2;					
Qy	6	AAUCUGAAGGGCGUAGGCCGAAAUACGG	38				
Db	6	ATTCTGATGAGGCCGTTAGGCCGAAAATCAG	38				
RESULT 25	AR330943	AR330943	38 bp	RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 4122 from Patent WO0193103.						
ACCESSION	AX218680	AX218680	38 bp	RNA	linear	PAT 07-SEP-2001	
VERSION	AX218680	AX218680.1	GI:15546404				
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE	1	synthetic construct					
AUTHORS	Blatt,L., McSwiggen,J. and Chowdhury,B.M.						
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogc gene expression						
JOURNAL	PATENT: WO 0159103-A 4122 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);						

FEATURES	McSwiggen, James (US) ; Chowrira, Bharat M. (US)	Location/Qualifiers	/db_xref="taxon:32630" /note="Nucleic Acid"
SOURCE	1. .38		
DEFINITION	/organism="synthetic construct"		
ACCESSION	/mol_type="unassigned RNA"		
VERSION	/db_xref="taxon:32630"		
KEYWORDS	/note="Nucleic Acid"		
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
ORIGIN			
Query Match	78.4%; Score 29.8; DB 6; Length 38;		
Best Local Similarity	72.7%; Pred. No. 0.065;		
Matches	24; Conservative 7; Mismatches 2; Indels 0; Gaps 0;		
Qy	2 CGGCAUCUGAUGAGGCCGUUAGGCCAAAU	34	
Db	2 CTGGATCTGAGGCGTTAGGCCAAAT	34	
RESULT 28			
AX218848	AX218848	38 bp	RNA
LOCUS	Sequence 4290 from Patent WO0159103.		
DEFINITION		Linear	PAT 07-SEP-2001
ACCESSION	AX218848		
VERSION	AX218848.1 GI:15546572		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
ORIGIN			
Query Match	78.4%; Score 29.8; DB 6; Length 38;		
Best Local Similarity	72.8%; Pred. No. 0.065;		
Matches	26; Conservative 5; Mismatches 2; Indels 0; Gaps 0;		
Qy	1 GCAAUUCUGAUGAGGCCGUUAGGCCAAAU	36	
Db	1 GCAACTGTGAGGGCGTTAGGCCGAAGACA	36	
RESULT 29			
AX219667	AX219667	38 bp	RNA
LOCUS	Sequence 5109 from Patent WO0159103.		
DEFINITION		Linear	PAT 07-SEP-2001
ACCESSION	AX219667		
VERSION	AX219667.1 GI:15547391		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
ORIGIN			
Query Match	78.4%; Score 29.8; DB 6; Length 38;		
Best Local Similarity	72.7%; Pred. No. 0.065;		
Matches	26; Conservative 7; Mismatches 2; Indels 0; Gaps 0;		
Qy	2 CGGCAUCUGAUGAGGCCGUUAGGCCAAAU	34	
Db	2 CTGGATCTGAGGCGTTAGGCCAAAT	34	
RESULT 30			
AX222419	AX222419	38 bp	RNA
LOCUS	Sequence 7861 from Patent WO0159103.		
DEFINITION		Linear	PAT 07-SEP-2001
ACCESSION	AX222419		
VERSION	AX222419.1 GI:15550143		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
ORIGIN			
Query Match	78.4%; Score 29.8; DB 6; Length 38;		
Best Local Similarity	72.7%; Pred. No. 0.065;		
Matches	26; Conservative 7; Mismatches 3; Indels 0; Gaps 0;		
Qy	4 GAAACTGATGAGGCCGTAGGCCAAATCAG	37	
Db	4 GAAACTGATGAGGCCGTAGGCCAAATCAG	37	
RESULT 31			
AR331511	AR331511	38 bp	RNA
LOCUS	Sequence 8913 from patent US 6566127.		
DEFINITION		Linear	PAT 17-AUG-2003
ACCESSION	AR331511		
VERSION	AR331511.1 GI:33717319		
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
ORIGIN			
Query Match	77.9%; Score 29.6; DB 6; Length 39;		
Best Local Similarity	72.2%; Pred. No. 0.08;		
Matches	26; Conservative 6; Mismatches 4; Indels 0; Gaps 0;		
Qy	1 .38		
Db	1 /organism="unassigned RNA"		
FEATURES			
SOURCE			

QY	1	CCUGCAUCUGAUGAGCCGUAAGGCCGAANAUCA	36				RESULT 34
Db	1	CGTGGAACTGTGTGAGGCCGTTAGGCCGAAGATCA	36				AX219601
LOCUS		AX219601		38 bp	RNA	linear	PAT 07-SEP-2001
DEFINITION		Sequence 5 043 from Patent WO0159103.					
ACCESSION		AX219601					
VERSION		AX219601.1					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
Source							
ORIGIN							
Query Match		77.9%; Score 29.6; DB 6; Length 38;					
Best Local Similarity		72.2%; Pred. No. 0; 08; Mismatches 6; Indels 0; Gaps 0;					
Matches							
QY	2	CUGCAUCUGAUGAGCCGTTAGGCCGAANAUCA	37				
Db	2	CTTCACCTGATGAGGCCGTTAGGCCGAAGCTCAG	37				
RESULT 33							
AX218873							
LOCUS		AX218873		38 bp	RNA	linear	PAT 07-SEP-2001
DEFINITION		Sequence 4315 from Patent WO0159103.					
ACCESSION		AX218873					
VERSION		AX218873.1					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
Source							
ORIGIN							
Query Match		77.9%; Score 29.6; DB 6; Length 38;					
Best Local Similarity		72.2%; Pred. No. 0; 08; Mismatches 6; Indels 0; Gaps 0;					
Matches							
QY	2	CUGCAUCUGAUGAGCCGTTAGGCCGAANAUCA	37				
Db	2	CTTCACCTGATGAGGCCGTTAGGCCGAAGCTCAG	37				
RESULT 34							
AX222613							
LOCUS		AX222613		38 bp	RNA	linear	PAT 07-SEP-2001
DEFINITION		Sequence 8 055 from Patent WO0159103.					
ACCESSION		AX222613					
VERSION		AX222613.1					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
Source							
ORIGIN							
Query Match		77.9%; Score 29.6; DB 6; Length 38;					
Best Local Similarity		72.2%; Pred. No. 0; 08; Mismatches 6; Indels 0; Gaps 0;					
Matches							
QY	3	UCCAAUCGAGAGCCGUUAGGCCAAAUACAG	38				
Db	3	TGGAATCTGATGAGGCCGTTAGGCCGAATAAG	38				
RESULT 35							
AX222613							
LOCUS		AX222613		38 bp	RNA	linear	PAT 07-SEP-2001
DEFINITION		Sequence 8 055 from Patent WO0159103.					
ACCESSION		AX222613					
VERSION		AX222613.1					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
Source							
ORIGIN							
Query Match		77.9%; Score 29.6; DB 6; Length 38;					
Best Local Similarity		72.2%; Pred. No. 0; 08; Mismatches 6; Indels 0; Gaps 0;					
Matches							
QY	3	UCCAAUCGAGAGCCGUUAGGCCAAAUACAG	38				
Db	3	TGGAATCTGATGAGGCCGTTAGGCCGAATAAG	38				
RESULT 36							
AX227899							

LOCUS	AX227899	DEFINITION Sequence 1271 from Patent WO0157206.	38 bp	RNA	Linear	PAT 10-SEP-2001	ORGANISM synthetic construct
DEFINITION		other sequences; artificial sequences.					REFERENCE other sequences; artificial sequences.
ACCESSION	AX227899						AUTHORS Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
VERSION	AX227899.1	GI:15557040					TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
KEYWORDS	.	synthetic construct					Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
SOURCE							Patent: WO 0211674-A 2711 14-FEB-2002;
ORGANISM		synthetic construct					RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
REFERENCE	1						Thompson, James (US)
AUTHORS	Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.						Location/Qualifiers
TITLE	Method and reagent for the inhibition of checkpoint kinase-1 (chk						1. .38
JOURNAL							/organism="synthetic construct"
FEATURES							/mol_type="unassigned RNA"
SOURCE							/db_xref="taxon:32630"
ORIGIN							/note="Enzymatic Nucleic Acid"
RESULT 37		Query Match	77.9%; Score 29.6; DB 6; Length 38;				
LOCUS	AX580764	Best Local Similarity	75.0%; Pred. No. 0.08;				
DEFINITION		Matches 27; Conservative 5; Mismatches 4; Indels 0; Gaps 0;					
ACCESSION	AX580764						
VERSION	AX580764.1	GI:27649966					
KEYWORDS	.						
SOURCE							
ORGANISM		synthetic construct					
REFERENCE	1	other sequences; artificial sequences.					
AUTHORS	Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.B.						
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)						
JOURNAL		Patent: WO 0211674-A 2602 14-FEB-2002;					
FEATURES		RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;					
SOURCE		Thompson, James (US)					
ORIGIN		Location/Qualifiers					
RESULT 38		Query Match	77.9%; Score 29.6; DB 6; Length 38;				
LOCUS	AX580873	Best Local Similarity	72.2%; Pred. No. 0.08;				
DEFINITION		Matches 26; Conservative 6; Mismatches 4; Indels 0; Gaps 0;					
ACCESSION	AX580873						
VERSION	AX580873.1	GI:27650075					
KEYWORDS	.						
SOURCE							
ORIGIN		synthetic construct					
RESULT 39		Query Match	77.9%; Score 29.6; DB 6; Length 38;				
LOCUS	AR330254	Best Local Similarity	72.2%; Pred. No. 0.08;				
DEFINITION		Matches 26; Conservative 6; Mismatches 4; Indels 0; Gaps 0;					
ACCESSION	AR330254						
VERSION	AR330254.1	GI:33716062					
KEYWORDS	.						
SOURCE							
ORGANISM		Unknown.					
REFERENCE	1	(bases 1 to 38)					
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.						
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor						
JOURNAL		Patent: US 6566127-A 7656 20-MAY-2003;					
FEATURES		Location/Qualifiers					
SOURCE		1. .38					
ORIGIN		/organism="unknown"					
RESULT 40		Query Match	77.4%; Score 29.4; DB 6; Length 38;				
LOCUS	AR330461	Best Local Similarity	80.6%; Pred. No. 0.098;				
DEFINITION		Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;					
ACCESSION	AR330461						
VERSION	AR330461.1	GI:33716269					
KEYWORDS	.						
SOURCE							
ORGANISM		Unknown.					
REFERENCE	1	(bases 1 to 38)					
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.						
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor						
JOURNAL		Patent: US 6566127-A 7853 20-MAY-2003;					
FEATURES		Location/Qualifiers					

Mon May 16 14:41:08 2005

us-09-927-046-2332.max.rge

Page 11

source
1. .38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN

Query Match 1. .38
Best Local Similarity 77.4%; Score 29.4; DB 6; Length 38;
Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AUUCUGAGCCGUNAGCGAAAUCA 36
Db 6 AACTGATGAGCCGTTAGGCCAAATCA 36

Search completed: May 13, 2005, 18:17:11
Job time : 1091.95 secs

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94 28.8 75.8 38 4 AAG96035
 95 28.8 75.8 38 4 AAG96344 Human Chk
 96 28.8 75.8 38 4 AAG96309 Human Chk
 97 28.8 75.8 38 4 ABP04054 Human NCG
 98 28.8 75.8 38 4 ABP04038 Human NCG
 99 28.8 75.8 38 4 ABP07775 Human CD2
 100 28.8 75.8 38 4 ABP04414 Human NCG

Abk04414 Human NCG

Db 1 cccggcaaucugaaucggaggccgtuaggccgaaaaucagg 38

ALIGNMENTS

RESULT 1

ABK57961

ID ABK57961 standard; RNA; 38 BP.

XX

AC

XX

DT 02-JUL-2002 (first entry)

XX

DR Human CLCA1 gene enzymatic nucleic acid #2332.

XX

KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.

KW Homo sapiens.

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PD 14-FEB-2002.

XX

PP 09-AUG-2001; 2001WO-US024970.

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PA (SYNT) SYNTEX USA LLC.

XX

PA (THOM/) THOMPSON J.

XX

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX

DR WPI; 2002-217145/27.

XX

PT Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

XX

PT channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

XX

PS Claim 5; Page 55; 152pp; English.

XX

CC The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

XX

Sequence 36 BP; 11 A; 8 C; 10 G; 0 T; 7 U; 0 Other;

SQ 94.7%; Score 36; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.8e-06; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 38; DB 6; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7.7e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ccougaaucaugaaugagccgtuaggccgaaaaucagg 38

Db 1 cccggcaaucugaaucggaggccgtuaggccgaaaaucagg 38

Qy 2 CUGCAUUCUGAAGGCCGUUAGCCGAAAUCA 37
CC leukaemia, HIV (human immunodeficiency virus) associated lymphoma (MCL), Immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NOGO sequence

XX Sequence 38 BP; 12 A; 8 C; 8 G; 0 T; 10 U; 0 Other;

Query Match 83.7%; **Score** 31.8; **DB** 4; **Length** 38;
Best Local Similarity 94.3%; **Pred.** No. 0 00042; **Mismatches** 2; **Indels** 0; **Gaps** 0;

Matches 33; **Conservative** 0;

DB

Qy 1 CUGCAUUCUGAAGGCCGUUAGCCGAAAUCA 36
CC 2 CUGCAUUCUGAAGGCCGUUAGCCGAAAUCA 36

XX Sequence 38 BP; 12 A; 8 C; 8 G; 0 T; 10 U; 0 Other;

Query Match 83.7%; **Score** 31.8; **DB** 4; **Length** 38;
Best Local Similarity 94.3%; **Pred.** No. 0 00042; **Mismatches** 2; **Indels** 0; **Gaps** 0;

Matches 33; **Conservative** 0;

DB

RESULT 3

ID ABBK04137

DE Human NOGO Hammerhead ribozyme substrate sequence #344.

XX 12-MAR-2002 (first entry)

AC ABBK04137;

XX Human; **ss**; antisense therapy; cytosstatic; antiinflammatory; haemostatic; cerebroprotective; nontropic; neuroprotective; antiparkinsonian; muscular; inozyme; G-cleaver; ambezyme; zinzyme; Lymphoma; Leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; Lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

PN

XX

PD 16-AUG-2001.

XX

PP 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-018179P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCsw/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

PT Blatt L, Mcswiggen J, Chowrira BM;

DR DR WPI; 2001-607195/69.

XX

PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., Lymphoma, leukemia, and PT central nervous system injury.

XX

PS Claim 89; Page 71; 200pp; English.

XX

CC The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down CC regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or an amberzyme (cleaving RNA with an NNN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

XX

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

PN

XX

PD 16-AUG-2001.

XX

PP 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-018179P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCsw/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

PT Blatt L, Mcswiggen J, Chowrira BM;

DR DR WPI; 2001-607195/69.

XX
Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.

XX
PS Claim 89; Page 74; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NGO). The
nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or
CC an amberzyme (cleaving RNA with an NN triplet), a zinzyme (cleaving RNA
with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC with a NGO motif. The CD20-targetting nucleic acid is used to cleave RNA
CC with a NGO motif. Furthermore, it may be contacted with a cell to reduce CD20 activity of
the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
therapies. In particular, the CD20 targetting nucleic acid may be used to
treat Lymphoma, Leukemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NGO-
targetting nucleic acid is used to cleave RNA of the NGO gene in the
presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
nucleic acid may be contacted with a cell to reduce NGO activity of the
cell and treat a patient having a condition associated with the level of
NGO. The treatment may further comprise the use of one or more
therapies. In particular, the NGO-targetting nucleic acid may be used to
treat central nervous system (CNS) injury and cerebrovascular accident
(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeld-Jakob
disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NGO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
based on the human NGO sequence

SQ sequence 38 BP; 11 A; 9 C; 11 G; 0 T; 7 U; 0 Other;

Query Match 82.6%; Score 31.4; DB 4; Length 38;
Best Local Similarity 97.0%; Pred. No. 0. 0.00063; Mismatches 0; Indels 0; Gaps 0;
Matches 32; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 5 CAUCAUCGAGGGCCGTAGCGGAAAUAGC 37
Db 5 CAUCAUGAGGCCGUUAGCCGAAAUAC 37

RESULT 5

ID ABL47321 Standard; RNA; 38 BP.

XX
AC ABL47321;
XX
DT 27-JUN-2003 (first entry)

XX
DR Human GRID hammerhead ribozyme oligonucleotide #49.
XX
KW Human; Grb2-related with Insert Domain; GRID; T-cell; ribozyme;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX
OS Homo sapiens.
XX
PN WO200162911-A2.
XX
PD 30-AUG-2001.
XX
PP 23-FEB-2001; 2001WO-US005957.

XX
PR 24-FEB-2000; 2000US-0184594P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

DR WPI; 2001-550088/61.

XX
PS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
molecules such as hammerhead ribozymes.

XX
PS Claim 5; Page 60; 108pp; English.

CC The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
for modulating the expression of GRID, to treat conditions such as
tissue/grat rejection and leukaemia. The oligonucleotides can also be
administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

SQ Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;

Query Match 82.6%; Score 31.4; DB 4; Length 38;
Best Local Similarity 97.0%; Pred. No. 0.00063; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCAAUUCUGAGGGCCGUUAGGCCGAAAUCA 36
Db 4 GCAGUCUGAGGCCGUUAGGCCGAAAUCA 36

RESULT 6

ID ABK57933 Standard; RNA; 38 BP.

AC ABK57933;

XX
DT 02-JUL-2002 (first entry)

XX
DB Human CLCA1 gene enzymatic nucleic acid #2304.

XX
Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.

XX
PN WO20021674-A2.

XX
PD 14-FEB-2002.

XX
PP 09-AUG-2001; 2001WO-US024970.

XX
PR 09-AUG-2000; 2000US-0224383P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grube A;

XX
DR WPI; 2002-217145/27.

XX
PT Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XX
 PS Claim 5; Page 55; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

SQ Sequence 38 BP; 11 A; 7 C; 10 G; 0 T; 10 U; 0 Other;
 Query Match 82.6%; Score 31.4; DB 6; Length 38;
 Best Local Similarity 97.0%; Pred. No. 0.0063; Mismatches 0; Indels 1; Gaps 0;
 Matches 32; Conservative 0; Miematches 1;

Qy 3 UGCAUCAUGAGGGGGGUAGGCCGAAAUUC 35
 Db 3 UGAAAUUCUGAUGAGGGGGGUAGGCCGAAAUC 35

RESULT 7
 ACDS2864
 ID ACDS2864 standard; RNA; 38 BP.
 XX
 AC ACDS2864;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV inozyme sequence #586.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyne;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotrophic; cytostatic;
 KW virucide; antiinflammatory; ss.
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PR 26-MAR-2002; 2002WO-US009187.
 PP
 XX
 PR 26-MAR-2001; 2001US-0081879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 24-OCT-2001; 2001US-0296876P.
 PR 05-DEC-2001; 2001US-0335059P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT-) BLATT L.
 PA (MACE-) MACEJAK D.
 PA (MCSE-) MCSWIGGEN J.
 PA (MORR-) MORRISSEY D.
 PA (PAVC-) PAVCO P.
 PA (LEEP-) LEE P.

PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Maciejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PT Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.

XX
 PT Novel compound useful for treating cirrhosis, liver failure, hepatitis C virus hepacellular carcinoma, or condition associated with hepatitis C virus infection.

PT
 XX
 PS Example 1; Page 161; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in the present invention

SQ Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;
 Query Match 82.6%; Score 31.4; DB 8; Length 38;
 Best Local Similarity 94.1%; Pred. No. 0.0063; Mismatches 2; Indels 0; Gaps 0;
 Matches 32; Conservative 0; Miematches 1;

Qy 1 CCUGCAUCUGAUGAGGCCGTAGSCGAAAU 34
 Db 1 CCGCAACACUGAGGAGGCCGUAGGCCGAAAU 34

RESULT 8
 ADM5641
 ID ADM5641 standard; RNA; 38 BP.
 XX
 AC ADM5641;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Hammerhead ribozyme targeting human GRID #49.
 XX
 KW Human; ss; GRID; Grid2-related with insert domain; hammerhead ribozyme; NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNAzyme; Inozyme; hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 US2003134806-A1.
 PN
 XX
 PD
 XX
 PR 23-FEB-2001; 2001US-00793818.
 PR 10-FEB-2000; 2000US-0181594P.
 XX
 PA (JARV/) JARVIS T.
 PA (CARL/) CARLOWITZ I V.
 PA (MCSE-) MCSWIGGEN J.
 PA (HAMB/) HAMBLIN P A.

PA (ELLI/) ELLIS J H.
 XX
 PT Jarvis T, Carlowitz IV, McSwiggen J, Hamblin PA, Ellis JH;
 XX DR
 WPI; 2003-829646/77.

PT New nucleic acid molecule that down-regulates expression of Grb2-related
 XX with insert domain (GRID) gene, useful for treating a condition
 associated with the level of GRID, e.g. tissue/graft rejection and
 leukaemia.

PS Claim 5; SEQ ID NO 954; 74pp; English.

XX The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNAzyme,
 CC including the novel nucleic acid molecule, reducing GRID activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC treating a patient having a condition associated with the level of GRID
 (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contracting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequences (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a hammerhead ribozyme of the invention.

XX Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;
 SQ

Query Match	82.6%	Score	31.4	DB	11;	Length	38;	
Best Local Similarity	97.0%	Pred.	No.	0.00063;	Mismatches	32;	Matches	32;
AC					Indels	0;	Gaps	0;
XX								

Qy 4 GCAUCUGAGGGCGGUAGGCCGAAAUCA 36
 Db 4 GCAUCUGAGGGCGGUAGGCCGAAAUCA 36

RESULT 9

ID	ADM1662	AC	ADM1662	DT	03-JUN-2004	XX
XX	Standard; RNA; 38 BP.			(first entry)		
AC						
XX						

DB Hepatitis B virus (HBV) enzymatic nucleic acid #1254.

XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
 KW virucide; hepatotropic; antinflammatory; cytostatic.
 XX OS Hepatitis B virus.

XX PN US2004054156-A1.

XX PD 18-MAR-2004.

XX PP 15-JAN-2003; 2003US-00342902.

XX PR 14-MAY-1992; 92US-00882712.

PR 07-FEB-1994; 94US-0193627.

PR 08-NOV-1999; 99US-00336430.

PR 20-MAR-2000; 2000US-00531025.

PR 09-AUG-2000; 2000US-00336385.

PR 24-OCT-2000; 2000US-00596347.

PR 08-JUN-2001; 2001US-00877478.

PA (DRAP/) DRAPER K.
 PA (BLAT/) BLATT L.
 PA (MCsw/) MCSWIGGEN J A.
 PA (MORR/) MORRISSEY D.
 XX PT Draper K, Blatt L, Mcswiggen JA, Morrissey D;
 DR DR
 XX PT Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
 PT specifically cleaving RNA derived from hepatitis B virus and comprising
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.
 XX PS Disclosure; SEQ ID NO 3796; 122pp; English.

XX The invention relates to an enzymatic nucleic acid molecule that
 CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
 CC comprising one or more binding arms, without requiring the presence of a
 CC 2'-OH group within the molecule for activity. The nucleic acids are
 CC useful for treating hepatitis B virus infection, hepatitis,
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
 CC combination with other therapies such as lamivudine and interferons. The
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and
 CC mutations within diseased cells, for detecting the presence of HBV RNA in
 CC a cell, for the study of RNA and for down-regulating gene expression of
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
 CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
 CC RNA of the invention. Note: The sequence data for this patent is also
 CC available in electronic format from USPTO at
 CC seqbeta.uspto.gov/sequence.html.

XX Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;
 SQ

Query Match	82.6%	Score	31.4	DB	12;	Length	38;	
Best Local Similarity	94.1%	Pred.	No.	0.00063;	Mismatches	32;	Matches	32;
AC					Indels	0;	Gaps	0;
XX								

Qy 1 CCUGCAAUCUGAGGGCGGUAGGCCGAAAU 34
 Db 1 CCUGCAAUCUGAGGGCGGUAGGCCGAAAU 34

RESULT 10

ID	ACN26747	AC	ACN26747	DT	22-APR-2004	XX
XX	Standard; RNA; 38 BP.			(first entry)		
AC						
XX						

DB WNV minus strand Hammerhead Ribozyme SEQ ID NO 26763.

XX WNV: West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW viricide; neuroprotective; antibacterial; replication; pancreaticitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX OS West Nile Virus.

XX PN WO20026637-A2.

XX PD 06-SEP-2002.

XX PP 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCsw/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX DR XX
 XX PT XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX PG XX
 XX Claim 24; SEQ ID NO 26763; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. Pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberryne and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention.
 XX SQ Sequence 38 BP; 11 A; 6 C; 13 G; 0 T; 8 U; 0 Other;
 XX
 Query Match 82.1%; Score 31.2; DB 6; Length 38;
 Best Local Similarity 91.7%; Pred. No. 0.00078;
 Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 CUCGCAUCAUGAGGCCGUUAGCCGAAACUAG 37
 Db 2 CGCGAGUCUGAUGAGGCCGUUAGCCGAAACAGCAG 37
 XX
 RESULT 11
 ID ACN2700
 ID ACN27300 standard; RNA; 38 BP.
 ACN27300;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 27316.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyne; ss.
 KW OS West Nile Virus.
 KW West Nile Virus.
 WO200208637-A2.
 XX
 DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 26266.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyne; ss.
 OS West Nile Virus.
 XX
 PP 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLATT/) BLATT L.
 PA (MCIGEN/) MCNIGGEN J A.
 PI Blatt L, Mcniggen JA;
 PI Blatt L, Mcniggen JA;
 DR WPT; 2002-706994/76.
 XX
 PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 24; SEQ ID NO 26266; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. Pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC

CC in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX	Sequence 38 BP; 12 A; 7 C; 14 G; 0 T; 5 U; 0 Other;
SQ	Query Match 80.5%; Score 30.6; DB 6; Length 38;
	Best Local Similarity 89.2%; Pred. No. 0.0014;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CUGCAUCAUCUGAUGAGGCCGCUUAGGCCGAAGAACUAGC 38	Db 2 CUGGAACTAGAUGAGCCGCUUAGGCCGAAGAGGG 38

RESULT 14

ACN27117	ID ACN27117 standard; RNA; 38 BP.
XX	
AC	ACN27117;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	WNV minus strand Hammerhead Ribozyme SEQ ID NO 27133.
XX	
KM	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.
KW	
OS	West Nile Virus.
XX	
PN	WO200268637-A2.
XX	
PD	06-SBP-2002.
XX	
PR	19-OCT-2001; 2001WO-US048350.
XX	
PR	20-OCT-2000; 2000US-0242411P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLATT L.) BLATT L.
PA	(MCSWIGEN J A.) MCSWIGEN J A.
XX	
PI	Blatt L, Mcswiggen JA;
PI	Blatt L, Mcswiggen JA;
DR	WPI; 2002-706994/76.
XX	
PT	New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX	
PS	Claim 24; SEQ ID NO 27133; 495pp; English.
XX	
CC	The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. Pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17505-17514 are given in the specification. The present sequence is that of a nucleic acid molecule of the invention
CC	Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;
CC	Query Match 80.5%; Score 30.6; DB 6; Length 38;
CC	Best Local Similarity 89.2%; Pred. No. 0.0014;
CC	Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CC	Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CC	Qy 2 CUGCAUCAUCUGAUGAGGCCGCUUAGGCCGAAGAACUAGC 38
CC	Db 2 CUGGAACTAGAUGAGCCGCUUAGGCCGAAGAGGG 38
CC	
SQ	

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.

XX WO200159103-A2.
 XX PD 16-AUG-2001.
 XX PP 0-9-FEB-2001; 2001WO-US004273.
 XX PR 1-1-FEB-2000; 2000US-0181797P.
 XX PR 2-8-FEB-2000; 2000US-0185516P.
 XX PR 0-6-MAR-2000; 2000US-0187128P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT-) BLATT L.
 PA (MCW-) MCSWIGGEN J.
 PA (CROW-) CROWIRA B M.
 PI Blatt L, Mcswiggen J, Chowira BM;
 XX DR WPI; 2001-607195/69.
 XX PS Claim 89; Page 75; 20pp; English.
 XX PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 CC expression of a CD20 gene and a nucleic acid molecule which down
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX
 XX
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-Cleaver (cleaving RNA with a NN motif),
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's Lymphoma (NHL), bulky, low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NGO-
 CC targetting nucleic acid is used to cleave RNA of the NGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 XX based on the human NGO sequence
 SQ Sequence 38 BP; 13 A; 9 C; 9 G; 0 T; 7 U; 0 Other;
 Query Match 80 0%; Score 30.4; DB 4; Length 38;
 Best Local Similarity 96.9%; Pred. No. 0.0018; Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 YY 5 CAUCUGAUGAGGCCGUAAGCCCGAAAUCA 36
 SQ Query Match 80 0%; Score 30.4; DB 6; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.0018; Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 YY 4 GCAUCUGAUGAGGCCGUAAGCCCGAAAUCA 36
 Db 4 GCAUCUGAUGAGGCCGUAAGCCCGAAAUCA 36
 RESULT 19
 ACN29362 standard; RNA; 38 BP.
 ID ACN29362;
 XX DT 22-APR-2004 (first entry)
 XX DE WNV minus strand Inozyme SEQ ID NO 29378.
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatic;
 XX encephalitis; myocarditis; meningitis; infection; hepatitis;
 XX liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;
 XX Amberzyme; Zinzyme; ss.
 XX OS West Nile Virus.
 XX PN WO200268637-A2.
 XX DR 06-SBP-2002.
 XX PD 19-OCT-2001; 2001WO-US048350.
 XX PT 20-OCT-2000; 2000US-0242411P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT-) BLATT L.
 PA (MCW-) MCSWIGGEN J A.
 PI Blatt L, Mcswiggen JA;
 XX DR WPI; 2002-706394/76.
 XX PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX PS Claim 24; SEQ ID NO 29378; 49pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 1502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX Sequence 38 BP; 11 A; 7 C; 11 G; 0 T; 8 U; 1 Other;
 Query Match 80 0%; Score 30.4; DB 6; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.0018; Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 YY 4 GCAUCUGAUGAGGCCGUAAGCCCGAAAUCA 36
 Db 4 GCAUCUGAUGAGGCCGUAAGCCCGAAAUCA 36
 RESULT 20
 ABK04516 standard; RNA; 38 BP.
 ID ABK04516
 XX

AC ABK04516;
 XX DT 12-MAR-2002 (first entry)
 DE Human Nogo Hammerhead ribozyme substrate sequence #723.
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nocropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead; ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyne; Lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocythaemia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury; multiple sclerosis;
 KW cerebrovascular accident; CVA; Alzheimer's disease; amyotrophic lateral sclerosis; ALS;
 KW chemotherapy-induced neuropathy; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.
 OS Synthetic.
 XX PN WO200159103-A2.
 XX PD 16-AUG-2001.
 XX PR 09-FEB-2001; 2001WO-US004273.
 XX PR 11-FEB-2000; 2000US-0181797P.
 XX PR 28-FEB-2000; 2000US-0185516P.
 XX PR 06-MAR-2000; 2000US-0187128P.
 XX PR (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX PI Blatt L, Mcswiggen J, Chowrira BM;
 XX DR WPI; 2001-607195/69.
 XX PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a Cd20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX PS Claim 89; Page 77; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a Cd20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (Nogo). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyne (cleaving RNA
 CC with a YCY motif). The Cd20-targetting nucleic acid is used to cleave RNA
 CC of Cd20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce Cd20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of Cd20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the Cd20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular non-Hodgkin's
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocythaemia, and inflammatory arthropathy. The Nogo
 CC targeting nucleic acid is used to cleave RNA of the Nogo gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with cell to reduce Nogo activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC Nogo. The treatment may further comprise the use of one or more
 CC therapies. In particular, the Nogo-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke) Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Crutzefeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of Nogo expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human Nogo sequence
 XX Sequence 38 BP; 13 A; 8 C; 10 G; 0 T; 7 U; 0 Other;
 SQ Query Match 79.5%; Score 30.2; DB 4; Length 38;
 DB Matches 32; Local Similarity 91.4%; Pred. No. 0.002; Mi matches 3; Indels 0; Gaps 0;
 QY 2 CUGCAUCAUGAAGGCCGUAGGCCGAAUA CA 36
 2 CUGCAACCUGAAGAGGCCGUAGGCCGAAAGUA 36
 RESULT 21
 ACN26549
 ID ACN26549 standard; RNA; 38 BP.
 XX AC ACN26549;
 XX DT 22-APR-2004 (first entry)
 XX DB WNV minus strand Hammerhead Ribozyme SEQ ID NO 26565.
 XX PR WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyne; SS.
 XX OS West Nile Virus.
 XX PN WO200268637-A2.
 XX PR 19-OCT-2001; 2001WO-US048350.
 XX PR 20-OCT-2000; 2000US-0242411P.
 XX PR (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCW/) MCSWIGGEN J A.
 XX PI Blatt L, Mcswiggen JA;
 XX DR WPI; 2002-706994/76.
 XX PS Claim 24; SEQ ID NO 26565; 495pp; English.
 CC The invention relates to nucleic acid molecules that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX PS Claim 24; SEQ ID NO 26565; 495pp; English.
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocardiitis, meningitis, neurological infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

QY	4	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38	DE	RESULT 22	2 CTGCAACTUGAGAGGCGUUGGCCGAAUACAG	37
Best Local Similarity	91.4%	Pred. No.	0.0022;	ID	ACN30394	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
Matches	32;	Conservative	0;	ID	ACN30394;	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
Db	4	GCAACUGAGGCGCGUAGGCCGAAUAGGAGG	38	AC	ACN30394;	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX				AC	ACN30394;	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
DT	22-APR-2004	(first entry)		XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX				XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
DE	WNV minus strand Inozyme SEQ ID NO 30410.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX				XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
DE	WNV: West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viricide; neuroprotective; antibacterial; replication; Pancratistis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme; Ambezyme; Zinzyne; ss.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX	West Nile Virus.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
OS				XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PN	W0200157206-A2.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PD	06-SEP-2002.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PD	19-OCT-2001; 2001WO-US048350.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PR	20-0CT-2000; 2000US-024241P.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PR	(RIBO-) RIBOZYME PHARM INC.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PA	(BLATT) BLATT L.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PA	(MCsw/) MCSWIGEN J A.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PI	Blatt L, McSwiggen JA;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX	XX			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PA	(RIBO-) RIBOZYME PHARM INC.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PA	(BLATT) BLATT L.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PA	(MCsw/) MCSWIGEN J A.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PT	WPI; 2002-70694/76.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PT	New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PT	WPI; 2002-70694/76.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PS	Claim 24; SEQ ID NO 30410; 495PP; English.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PS	The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNzyme, Ambezyme and Zinzyne. The nucleic acid molecules further comprise at least five nucleotides, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and SEQ ID NO 1705-17514 are given in the specification. The present sequence is that of a nucleic acid molecule of the invention.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
PS	Sequence 38 BP; 9 A; 9 C; 11 G; 0 T; 8 U; 1 Other;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
Query Match	79.5%	Score	30.2;	DB	RESULT 24	2 CTGCAACTUGAGAGGCGUUGGCCGAAUACAG	37
Best Local Similarity	86.8%	Pred. No.	0.0026;	ID	ABK58289	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
Matches	33;	Conservative	0;	ID	ABK58289	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
QY	1	CUGCAACUGAUCAGGAGGCCGUUGGCCGAAUACGG	38	AC	ABK58289;	GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
Db	1	CUGCCCAUCUGAUCAGGAGGCCGUUGGCCGAAUACGG	38	XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX				XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
DT	02-JUL-2002 (first entry)			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
XX				XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
DE	Human CLCA gene enzymatic nucleic acid #2660.			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
KW	Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
KW	antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
KW	chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38
KW	oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;			XX		GCAUTGAGGGCCGTUAGGCCGAAUACGG	38

PR	20-OCT-2000;	2000US-024241P.
XX		
XX	(RIBO-)	RIBOZYME PHARM INC.
PA	(BLATT/)	BLATT L.
PA	(BLATT/)	BLATT L.
PA	(MCSEN/)	MCSWIGGEN J A.
PA	(MCSEN/)	MCSWIGGEN J A.
PI	Blatt L.	Mcswiggen JA;
XX		
DR	WPI;	2002-706994/76.
XX		
PT	New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.	
PT	New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.	
PS	Claim 24; SEQ ID NO 26160; 495pp; English.	
XX		
CC	The invention relates to nucleic acid molecules that modulate replication of the West Nile virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule, Hammerhead, Inzyme, G-cleaver, DNAzyme, Ambergyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose linkages on at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 219-2206 and 1750-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention.	
CC	Sequence 38 BP; 10 A; 9 C; 10 G; 0 T; 9 U; 0 Other;	
CC	Query Match 78.9%; Score 30; DB 6; Length 38;	
CC	Best Local Similarity 86.8%; Pred. No. 0.0026;	
CC	Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
CC	QY 1 CCUGCAUCUGAGGACCGUAGGCCAAAUACAGG 38	
CC	DB 1 CGUGCAUCUGAGGACCGUAGGCCGAACACAGG 38	
XX		
RESULT 27		
ID	ACD50521 standard; RNA; 38 BP.	
XX		
AC	ACD50521;	
XX		
DT	23-SEP-2003 (first entry)	
XX		
DE	HBV hammerhead ribozyme sequence #89.	
XX		
Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inzyme; zinzyne; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; viricide; antiinflammatory; ss.		
XX		
OS	Hepatitis B virus.	
XX		
PN	WO200281494-A1.	
XX		
PD	17-OCT-2002.	
XX		
PF	26-MAR-2002; 2002WO-US009187.	
XX		
PR	26-MAR-2001; 2001US-00817879.	
PR	08-JUN-2001; 2001US-00877478.	
PR	24-OCT-2001; 2001US-033505PP.	
XX		
RESULT 28		
ID	ADL53551 standard; RNA; 38 BP.	
XX		
AC	ADL53551;	
XX		
DT	20-MAY-2004 (first entry)	
XX		
DE	Human IKK-gamma ribozyme sequence #29.	
XX		
KW	anti-sense oligonucleotide; neurite growth inhibitor; NOGO; protaglandin D2 receptor; PTGDR; IkappaB kinase; IKK; protein kinase PKR; cerebrovascular accident; central nervous system injury; CNS injury; spinal cord injury; cancer; melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis; restenosis; asthma; Crohn's disease; diabetes; obesity; autoimmune disease; lupus; multiple sclerosis; transplant rejection; graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis; allergy; asthma; allergic rhinitis; atopic dermatitis; IKK-gamma ribozyme; substrate; ss; human.	

XX
OS Homo sapiens.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PP 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 28-AUG-2001; 2001US-031515P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowkira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 57; SEQ ID NO 7084; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/grafft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human IKK- gamma ribozyme sequence.
XX
SQ Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 8 U; 0 Other;
Query Match 78.9%; Score 30; DB 11; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0026;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGUCGAUCAUAGAAGCGCUAGGGAGAAAUACGAG 38
Db 1 CGUGUCUCAUAGAAGCGCUAGGGAGAAAUACGAG 38
XX
RESULT 29
ADLS5719
XX
AC ADLS5719;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR ribozyme sequence #183.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostanandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atop dermatitis; PKR ribozyme;
KW substrate; ss; human.
XX
XX
OS Homo sapiens.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PP 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-029412P.
PR 28-AUG-2001; 2001US-031315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowkira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 57; SEQ ID NO 9252; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/grafft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR ribozyme sequence.
XX
SQ Sequence 38 BP; 11 A; 7 C; 8 G; 0 T; 12 U; 0 Other;
Query Match 78.9%; Score 30; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 AAUCGAUAGGCCCTAAC3CCGAAAU 35
Db 6 AAUCGAUAGGCCCTAAC3CCGAAAU 35
XX
RESULT 30
ADM60497
ID ADM60497 standard; RNA; 38 BP.
XX
AC ADM60497;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) enzymatic nucleic acid #89.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotrophic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US200404156-A1.
XX
PD 18-MAR-2004.

XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 PP Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 PR 14-MAY-1932; 92US-00882712.
 PR 07-FEB-1934; 94US-00193627.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-006385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 XX
 PA (DRAP/) DRAPER K.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (MORR./) MORRISSEY D.
 XX
 PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
 PT
 XX
 DR WPI; 2004-247781/23.
 XX
 PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
 specifically cleaving RNA derived from hepatitis B virus and comprising
 one or more binding arms, useful for treating hepatitis and cirrhosis.
 XX
 PS Disclosure; SEQ ID NO 2631; 122pp; English.
 XX
 CC The invention relates to an enzymatic nucleic acid molecule that
 specifically cleaves RNA derived from hepatitis B virus (HBV) and
 comprising one or more binding arms, without requiring the presence of a
 CC 2'-OH group within the molecule for activity. The nucleic acids are
 useful for treating hepatitis B virus infection, hepatitis,
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
 combination with other therapies such as lamivudine and interferons. The
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and
 mutations within diseased cells, for detecting the presence of HBV RNA in
 a cell, for the study of RNA and for down-regulating gene expression of
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
 CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
 CC RNA of the invention. Note: The sequence data for this patent is also
 available in electronic format from USPTO at
 CC Seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
 Query Match 78.9%; Score 30; DB 12; Length 38;
 Best Local Similarity 86.8%; Pred. No. 0 0026; Mismatches 5; Indels 0; Gaps 0;
 Matches 33; Conservative 0;
 Qy 1 CGUGCAUUCUGAGGAGCCGGUAGGCCGAAGAUACAGG 38
 Db 1 CGAACAAAGCUGAGGAGCCGGUAGGCCGAAGAUAGGG 38
 RESULT 31
 ABK07861
 ID ABK07861 standard; RNA; 38 BP.
 XX
 AC ABK07861;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Hammerhead ribozyme substrate sequence #104.
 XX
 Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nortropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleavers; ambrizyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW NCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200159103-A2.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-018516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 central nervous system injury.
 XX
 PS Claim 31; Page 141; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL); myeloid, low-grade or follicular NHL; lymphocytic
 CC leukaemia; HIV (human immunodeficiency virus) associated NHL; mantle-cell
 CC lymphoma (NCL); immunocytoma (IMC); small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human CD20 sequence
 XX
 SQ Sequence 38 BP; 11 A; 8 C; 10 G; 0 T; 9 U; 0 Other;
 Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0 0032; Mismatches 2; Indels 0; Gaps 0;
 Matches 31; Conservative 0;

Db	2	CCTCUAAUCUGAUGGCCGUNAGGCCGAAAU	34
RESULT 32			
ID	ABK04290		
XX	ABK04290 standard; RNA; 38 BP.		
AC	ABK04290;		
XX	12-MAR-2002 (first entry)		
XX	Human NOGO Hammerhead ribozyme substrate sequence #497.		
XX	Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; Lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Parkinson's disease; muscular dystrophy; neurodegenerative disease.		
OS	Homo sapiens.		
XX	Synthetic.		
PN	W0200159103-A2.		
XX	16-AUG-2001..		
PP	09-FEB-2001; 2001WO-US004273.		
XX			
PR	11-FEB-2000; 2000US-0181797P.		
PR	28-FEB-2000; 2000US-018516P.		
PR	06-MAR-2000; 2000US-0187128P.		
XX	RIBOZYME PHARM INC.		
PA	(BLAT/) BLATT L.		
PA	(MCsw/) MCswiggen J.		
PA	(CHOW/) Chowrira B M.		
XX			
PI	Blatt L, Mcswiggen J, Chowrira BM;		
XX	WPI; 2001-607195/69.		
PT	Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.		
XX			
PS	Claim 89; Page 73; 20pp; English.		
XX			
CC	The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Enzyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif), a G-Cleaver (cleaving RNA with an NGN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zymase (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with CD20 in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodkin's lymphoma (NHL), bulky, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-		
CC	targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotheraphy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NOGO sequence		
CC	Sequence 38 BP; 11 A; 9 C; 13 G; 0 T; 5 U; 0 Other;		
CC	Best Local Similarity 93.9%; Pred. No. 0.0032; Length 38; Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	4 GCAUUCUGAUCAGGGCGUAGGCCGAAAUCA 36		
Db	4 GCAUUCUGAUCAGGGCGUAGGCCGAAAUCA 36		
RESULT 33			
ID	ABK04122		
XX	ABK04122 standard; RNA; 38 BP.		
AC	ABK04122;		
XX	12-MAR-2002 (first entry)		
DE	Human NOGO Hammerhead ribozyme substrate sequence #329.		
XX	Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inzyme; G-cleaver; amberzyme; zymase; Lymphoma; Leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; Lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; ALS; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.		
OS	Homo sapiens.		
XX	Synthetic.		
PN	W0200159103-A2.		
XX	16-AUG-2001.		
XX	09-FEB-2001; 2001WO-US004273.		
XX			
PR	11-FEB-2000; 2000US-0181797P.		
PR	28-FEB-2000; 2000US-0185516P.		
PR	06-MAR-2000; 2000US-0187128P.		
XX	RIBOZYME PHARM INC.		
PA	(BLAT/) BLATT L.		
PA	(MCsw/) MCswiggen J.		
PA	(CHOW/) Chowrira B M.		
XX			
PI	Blatt L, Mcswiggen J, Chowrira BM;		
XX	WPI; 2001-607195/69.		
PT	Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite		

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 89; Page 71; 20pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore,
 CC it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX Sequence 38 BP; 8 A; 8 C; 10 G; 0 T; 12 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0_0032; Mismatches 0; Indels 0; Gaps 0;

Matched 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGGCAACVUGAGGGCGGUAGGCCGAATAU 34
 Db 2 CUGGCAUCUGAAGAGGCCGUAGGCCGAATAU 34

RESULT 34

ID ABK05109 standard; RNA; 38 BP.

XX ABK05109;

AC ABK05109;

XX DT 12-MAR-2002 (first entry)

XX Human NOGO Inozyme substrate sequence #566.

XX Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nontropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hampered; ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.

OS Synthetic.
 XX
 PN WO20159103-A2.
 XX
 PD 16-AUG-2001.
 XX PR 09-FEB-2001; 2001WO-US004273.
 XX PR 11-FEB-2000; 2000US-018179P.
 XX PR 28-FEB-2000; 2000US-0185516P.
 XX PR 06-MAR-2000; 2000US-0187128P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLATT) BLATT L.
 PA (MCWIGGEN) MCWIGGEN J.
 PA (CHOWRI) CHOWRIRA B M.
 XX PI Blatt L, Mcswiggen J, Chowrira BM;
 XX DR WPI; 2001-607195/69.
 XX PR The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore,
 CC it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX Sequence 38 BP; 13 A; 6 C; 10 G; 0 T; 8 U; 1 Other;

Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 91.2%; Pred. No. 0_0032; Mismatches 3; Indels 0; Gaps 0;

Matched 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCAACUCAUGAGGCCGUAGGCCGAATAU 37
 Db 4 GAAACUGAAGGCCGUAGGCCGAATAU 37

RESULT 35

ACN26108
ID ACN26108 Standard; RNA; 38 BP.
XX
AC ACN26108;
XX DT 22-APR-2004 (first entry)
XX DB WNV minus strand Hammerhead Ribozyme SEQ ID NO 26124.
XX KW WNV; West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
KW Amberzyme; Zinzyne; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PP 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PT 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (BLATT) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PT Blatt L, Mcswiggen JA;
XX DR WPI; 2002-706994/76.
XX PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 24; SEQ ID NO 26124; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention. The present sequence is that of a nucleic acid
XX SQ Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;
SQ Sequence 38 BP; 14 A; 9 C; 9 G; 0 T; 6 U; 0 Other;
SQ Query Match 78.4%; Score 29.8; DB 6; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0032;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 6 AAUCUGAUGAGGCCGUAGCGAAAUACGG 38
Db 6 AAUCUGAUGAGGCCGUAGCGAAACUCAGG 38
RESULT 36
ACN27859
ID ACN27859 standard; RNA; 38 BP.
XX AC ACN27859;
XX DT 22-APR-2004 (first entry)
XX KW HBV hammerhead ribozyme sequence #105.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyne;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;

AC ADL5345;
 XX
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-0087478.
 PR 08-JUN-2001; 2001US-0296976P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 OS
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLATT/) BLATT L.
 PA (MACEJAK/) MACEJAK D.
 PA (MC_SWI/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P,
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 CC Novel compound useful for treating cirrhosis, liver failure, or
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1: Page 138; 387pp; English.

The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C Virus (HCV) or Hepatitis B Virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, RNazymes, zinzyymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression, such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents one of the HBV ribozyme, RNzyme, G-cleaver, zinzyne, DNAzyme or amberzyme sequences disclosed in the present invention.

Sequence 38 BP; 11 A; 8 C; 13 G; 0 T; 6 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 8; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.0032; Mismatches 0;
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAGGAGCCGTUAGGCCAAMA 33
 Db 1 CCUGGAUCUGAGGAGGCCGTUAGGCCGAAGA 33

Sequence 38 BP; 13 A; 8 C; 11 G; 0 T; 5 U; 1 Other;

Query Match 78.4%; Score 29.8; DB 11; Length 38;
 Best Local Similarity 91.2%; Pred. No. 0.0032; Mismatches 3;
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Qy 4 GCAUCUGAGGAGCCGTUAGGCCAAMAUCAG 37
 Db 4 GCAAACUGAUAGGGCGTGUAGGCCGAANBACCA 37

AC ADL5345;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR ribozyme sequence #809.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; Gloma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; PKR ribozyme;
 KW substrate; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00821735.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haebel P, Mcswiggen J, Posnauh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
 PT
 XX
 PS Claim 57; SEQ ID NO 9878; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemic/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR ribozyme sequence.

Sequence 38 BP; 13 A; 8 C; 11 G; 0 T; 5 U; 1 Other;

Query Match 78.4%; Score 29.8; DB 11; Length 38;
 Best Local Similarity 91.2%; Pred. No. 0.0032; Mismatches 3;
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Qy 4 GCAUCUGAGGAGCCGTUAGGCCAAMAUCAG 37
 Db 4 GCAAACUGAUAGGGCGTGUAGGCCGAANBACCA 37

RESULT 38
 ADL5345
 ID ADL5345 standard; RNA; 38 BP.
 XX

RESULT 39
 ADM60513
 ID ADM60513 standard; RNA; 38 BP.
 XX

AC ADM60513; AC ABX0648;

XX DT 03-JUN-2004 (first entry) XX DT 23-DBC-2002 (first entry)

DE Hepatitis B virus (HBV) enzymatic nucleic acid #105. DE HCV hammerhead ribozyme #821 for Hepatitis C virus substrate #821.

XX KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma; HCV ribozyme; HCV expression; HCV replication; cirrhosis; Virucide; KW cirrhosis; liver failure; lamivudine; interferon; genetic drift; type I interferon; interferon alpha; interferon beta; cytostatic; KW virucide; hepatotropic; antiinflammatory; cytostatic; KW贺状病毒; HBV; ss; 酶性核酸酸; RNA切割; KW interferon gamma; consensus interferon; hepatotrophic; antiinflammatory; hammerhead ribozyme; HH ribozyme; ss.

OS Hepatitis B virus. OS Hepatitis C virus.

XX PN US2004054156-A1. PN US2002082225-A1.

XX PD 18-MAR-2004. PD 27-JUN-2002.

PP 15-JAN-2003; 2003US-00342902. PP 23-MAR-1999; 99US-00274553.

XX PR 07-FEB-1994; 94US-00193627. PR 23-MAR-1999; 99US-00274553.

PR 08-NOV-1999; 99US-00436430. XX (BLAT/) BLATT L.

PR 20-MAR-2000; 2000US-00531025. PA (MCSW/) MCSWIGGEN J A.

PR 09-AUG-2000; 2000US-00639385. PA (ROBE/) ROBERTS B.

PR 24-OCT-2000; 2000US-00693347. PA (PAVC/) PAVCO P A.

PR 08-JUN-2001; 2001US-00877478. PA (MACE/) MACEJACK D.

XX (BLAT/) BLATT L. PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejjack D;

PA (MCSW/) MCSWIGGEN J A. DR XX

PA (ROBE/) ROBERTS B. DR WPI; 2002-617759/66.

PA (PAVC/) PAVCO P A. PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral

PT specifically cleaving RNA derived from hepatitis B virus and comprising PT replication and are useful for treating hepatitis and cirrhosis.

PT one or more binding arms, useful for treating hepatitis and cirrhosis. PT Disclosure; SEQ ID NO 2647; 122pp; English.

XX The invention relates to an enzymatic nucleic acid molecule that PT specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a PT 2'-OH group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis.

XX hepatocellular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

CC Sequence 38 BP; 11 A; 8 C; 13 G; 0 T; 6 U; 0 Other; CC Sequence 36 BP; 9 A; 9 C; 12 G; 0 T; 6 U; 0 Other;

CC Query Match 78.4%; Score 29.8; DB 12; Length 38; CC Query Match 77.9%; Score 29.6; DB 6; Length 36;

CC Best Local Similarity 93.9%; Pred. No. 0.0032; Pred. No. 0.0039; CC Best Local Similarity 88.9%; Pred. No. 0.0039; Pred. No. 0.0039;

CC Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0; CC Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCUGCAUCUTGAAGAGGCCGAGCGAAAAA 33 QY 2 CCUGCAUCUTGAAGAGGCCGAGCGAAAUACAG 37

Db 1 CGCGAACUTGAAGAGGCCGAGCGAAACGUCAG 36

RESULT 40

ABK02648

ID ABK02648 standard; RNA; 36 BP.

XX Job time : 202.173 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:59:31 ; Search time 93.9636 Seconds

(without alignments)
661.730 Million cell updates/sec

Title: US-09-927-046-2332
Perfect score: 38
Sequence: 1 ccugcaaucugaugaggccguuaggccggaaaaucagg 38

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA:
1: /cggn2_5/prodata/1/na/5A_COMB_seq: *
2: /cggn2_5/prodata/1/na/5B_COMB_seq: *
3: /cggn2_5/prodata/1/na/6A_COMB_seq: *
4: /cggn2_5/prodata/1/na/6B_COMB_seq: *
5: /cggn2_5/prodata/1/na/PCTUS_Comb_seq: *
6: /cggn2_5/prodata/1/na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31.2	82.1	38 4 US-09-371-772B-8998	Sequence 8998, AP
2	31.2	82.1	38 4 US-09-371-772B-9385	Sequence 9385, AP
3	30.8	81.1	38 4 US-09-371-772B-7472	Sequence 7472, AP
4	30.8	81.1	38 4 US-09-371-772B-8673	Sequence 8673, AP
5	30.6	80.5	38 4 US-09-371-772B-9574	Sequence 9574, AP
6	30.4	80.0	38 4 US-09-371-772B-9413	Sequence 9413, AP
7	30.4	80.0	38 4 US-09-371-772B-10563	Sequence 10563, AP
8	79.5	38 4 US-09-371-772B-843	Sequence 843, AP	
9	30	78.9	38 4 US-09-371-772B-526	Sequence 7526, AP
10	30	78.9	38 4 US-09-371-772B-766	Sequence 776, AP
11	30	78.9	38 4 US-09-371-772B-9339	Sequence 9339, AP
12	29.8	78.4	38 4 US-09-371-772B-8240	Sequence 8240, AP
13	29.8	78.4	38 4 US-09-371-772B-8345	Sequence 8345, AP
14	29.8	78.4	38 4 US-09-371-772B-8330	Sequence 8143, AP
15	29.6	77.9	38 4 US-09-371-772B-8913	Sequence 8913, AP
16	29.4	77.4	38 4 US-09-371-772B-7656	Sequence 7656, AP
17	29.4	77.4	38 4 US-09-371-772B-8663	Sequence 8663, AP
18	29.4	77.4	38 4 US-09-371-772B-8422	Sequence 8422, AP
19	29.4	77.4	38 4 US-09-371-772B-8953	Sequence 8953, AP
20	29.4	77.4	38 4 US-09-371-772B-9507	Sequence 9507, AP
21	29.4	77.4	38 4 US-09-371-772B-9559	Sequence 9559, AP
22	29.4	77.4	38 4 US-09-371-772B-11300	Sequence 11300, AP
23	29.2	76.8	38 1 US-08-373-124A-1154	Sequence 1754, AP
24	29.2	76.8	38 1 US-08-373-628-1754	Sequence 1754, AP
25	29.2	76.8	38 4 US-09-371-772B-8298	Sequence 8298, AP
26	29.2	76.8	38 4 US-09-371-772B-8707	Sequence 8707, AP
27	29.2	76.8	38 4 US-09-371-772B-9621	Sequence 9621, AP
28	76.8	38 4 US-09-371-772B-11279	Sequence 11279, AP	

Best Local Similarity 91.7%; Pred. No. 4.9e-05; Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 1
US-09-371-772B-8898

; Sequence 8898, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: Stinchcomb, Jim

; APPLICANT: Escobedo, Jaime

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00_876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 8898

; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Best Local Similarity 91.7%; Pred. No. 4.9e-05; Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
US-09-371-772B-7472

; Sequence 7472, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00_876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 7472

; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Best Local Similarity 91.7%; Pred. No. 4.9e-05; Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2
US-09-371-772B-9385

; Sequence 9385, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00_876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 9385

; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Best Local Similarity 91.7%; Pred. No. 4.9e-05; Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 4
US-09-371-772B-8673

; Sequence 8673, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; APPLICANT: McSwiggen, Pam

; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00_876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 8673

; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8673

Query Match 81.1%; Score 30.8; DB 4; Length 38;

Best Local Similarity 94.1%; Pred. No. 7.5e-05; Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAAUUCUGAGGAGCCGUAGGCCGAANAU 34
Db 1 CCUGCAAGCUGAUGAGGCCGUAGGCCGAAAUU 34

RESULT 5

US-09-371-772B-9574

Sequence 9574, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0SEQ ID NO 9574
LENGTH: 38TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 80.5%; Score 30.6; DB 4; Length 38;
Best Local Similarity 89.2%; Pred. No. 9.3e-05; Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;Qy 2 CGCGCAUUCUGAGGAGCCGUAGGCCGAANAU CAGG 38
Db 2 CCUGCAUUCUGAGGAGCCGUAGGCCGAANAU CAGG 38

RESULT 6

US-09-371-772B-9413

Sequence 9413, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00_876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0SEQ ID NO 9413
LENGTH: 38

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-9413

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 96.9%; Pred. No. 0.00012; Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGCAUUCUGAGGAGCCGUAGGCCGAANAU CAGG 32
Db 1 CCUGCAAGCUGAUGAGGCCGUAGGCCGAAAU 32

RESULT 7

US-09-371-772B-10563

Sequence 10563, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0SEQ ID NO 10563
LENGTH: 38TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 96.9%; Pred. No. 0.00012; Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AUCUGAUGAGGCCGUAGGCCGAANAU CAGG 38
Db 7 AGCUGAUGAGGCCGUAGGCCGAANAU CAGG 38

RESULT 8

US-09-371-772B-8143

Sequence 8143, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00_876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0SEQ ID NO 8143
LENGTH: 38

TYPE: RNA

PRIOR APPLICATION NUMBER: US 60/005, 974
 PRIOR FILING DATE: 1995-10-26
 CURRENT APPLICATION NUMBER: US 08/584, 040
 PRIOR APPLICATION NUMBER: US 60/005, 974
 PRIOR FILING DATE: 1995-10-26
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 8240
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8340

Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.00022; 2; Mismatches
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Oy	Db	6	AACUCGAGGCGGUAGGCCGAAGAUCAG	38
		6	AUTCUGAUGCAGGCCGUAGGCCGAAGAUCAG	38

RESULT 13

Sequence 8345, Application US/09371-772B
 Patent No.: 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00_876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005, 974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584, 040

PRIOR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14,225

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 8345

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8345

Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.00022; 2; Mismatches
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Oy	Db	6	AACUCGAGGCGGUAGGCCGAAGAUCAG	38
		6	AUTCUGAUGCAGGCCGUAGGCCGAAGAUCAG	38

RESULT 14

Sequence 8350, Application US/09371-772B
 Patent No.: 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

US-09-371-772B-8530

Query Match 78.4%; Score 29.8; DB 4; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.00022; 2; Mismatches
 Matches 31; Conservative 0; Indels 0; Gaps 0;

Oy	Db	2	CUGCAUCUGAUGCAGGCCGUAGGCCGAAGAU	34
		2	CUGAAUCAUCUGAUGCAGGCCGUAGGCCGAAGAU	34

RESULT 15

Sequence 8913, Application US/09371-772B
 Patent No.: 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00_876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005, 974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584, 040

PRIOR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14,225

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 8913

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8913

Query Match 77.9%; Score 29.6; DB 4; Length 38;
 Best Local Similarity 88.9%; Pred. No. 0.00027; 4; Mismatches
 Matches 32; Conservative 0; Indels 0; Gaps 0;

Oy	Db	1	CCUGCAUCUGAUGCAGGCCGUAGGCCGAAGAUC	36
		1	CCUGGAUCAUCUGAUGCAGGCCGUAGGCCGAAGAUC	36

RESULT 16

Sequence 7656, Application US/09371-772B
 Patent No.: 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

US-09-371-772B-7656

Query Match 77.9%; Score 29.6; DB 4; Length 38;
 Best Local Similarity 88.9%; Pred. No. 0.00027; 4; Mismatches
 Matches 32; Conservative 0; Indels 0; Gaps 0;

Oy	Db	1	CCUGCAUCUGAUGCAGGCCGUAGGCCGAAGAUC	36
		1	CCUGGAUCAUCUGAUGCAGGCCGUAGGCCGAAGAUC	36

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/371,772B
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7656
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7656

Query Match Best Local Similarity 77.4%; Score 29.4; DB 4; Length 38;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	7 AUCUGAUGAGGCGGAGGCGCAAAUACAG 37
Db	7 ACUGAUGAGGCCGUAGGGCCAAAUCAG 37

RESULT 17
 US-09-371-772B-7863
 Sequence 7863, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00,876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 7863
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7863

Query Match Best Local Similarity 77.4%; Score 29.4; DB 4; Length 38;
 Matches 30; Conservative 0; Mismatch 1; Indels 0; Gaps 0;

Qy	6 AACUGAUGAGGCGGAGGCGCAAAUCA 36
Db	6 AACUGAUGAGGCCGUAGGGCCAAAUC 36

RESULT 18
 US-09-371-772B-8422
 Sequence 8422, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8422
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8422

Query Match Best Local Similarity 77.4%; Score 29.4; DB 4; Length 38;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 CCTUGGAUTGAGGCGGAGGCGGUAGGCCGAA 31
Db	1 CCTUGCAAGTGAUGAGGCCGUAGGCCGAA 31

RESULT 20
 US-09-371-772B-9507
 Sequence 9507, Application US/09371772B
; Sequence 9507, Application US/09371772B

PATENT NO. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00,876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 9507
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-371-772B-9507
 Query Match 77.4%; Score 29.4; DB 4; Length 38;
 Best Local Similarity 96.8%; Pred. No. 0.00034; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 UCGUGAUGAGGCCGUUAGGCCGAAAUACAGG 38
 DB 8 UCGUGAUGAGGCCGUUAGGCCGAAAUACAGG 38
 RESULT 21
 US-09-371-772B-9559
 Sequence 9559, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Escobedo, Jaime
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Bacoone, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00,876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 11300
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 NAME/KEY: misc_feature
 LOCATION: (31)..(31)
 OTHER INFORMATION: n stands for inosine
 US-09-371-772B-11300
 Query Match 77.4%; Score 29.4; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00034; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCGUGCAUCUGAUGAGCCGCUUAGGCCGAA 32
 DB 1 CCGUGCAUCUGAUGAGCCGCUUAGGCCGAA 32
 RESULT 23
 US-08-373-124A-1754
 Sequence 1754, Application US/08373124A
 Patent No. 5646042
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Draper, Kenneth
 APPLICANT: McSwiggen, Jamie
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZIMES
 NUMBER OF SEQUENCES: 2627
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/373,124A
 FILING DATE: January 13, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/245,466

RESULT 22
 US-09-371-772B-11300
 Sequence 11300, Application US/09371772B
 Patent No. 6566127
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00,876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 11300
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 NAME/KEY: misc_feature
 LOCATION: (31)..(31)
 OTHER INFORMATION: n stands for inosine
 US-09-371-772B-11300
 Query Match 77.4%; Score 29.4; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00034; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCGUGCAUCUGAUGAGCCGCUUAGGCCGAA 32
 DB 1 CCGUGCAUCUGAUGAGCCGCUUAGGCCGAA 32

FILING DATE: May 18, 1994
 APPLICATION NUMBER: 08/152, 943
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: 07/987, 132
 FILING DATE: December 7, 1992
 APPLICATION NUMBER: 07/936, 422
 FILING DATE: August 26, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32, 327
 REFERENCE/DOCKET NUMBER: 209/035
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1754:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-373-124A-1754

Query Match Best Local Similarity 91.2%; Score 29.2; DB 1; Length 38; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
 US-08-435-628-1754
 ; Sequence 1754, Application US/08435628
 ; Patent No. 5817796
 ; GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Drapir, Kenneth
 APPLICANT: McSwiggen, James
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZIMES
 NUMBER OF SEQUENCES: 2627
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 513 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/435, 628
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/373, 124
 FILING DATE: January 13, 1995
 APPLICATION NUMBER: 08/245, 466
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 08/192, 943
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: 07/987, 132
 FILING DATE: December 7, 1992
 APPLICATION NUMBER: 07/936, 422

Query Match Best Local Similarity 91.2%; Score 29.2; DB 1; Length 38; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
 US-08-435-628-1754
 ; Sequence 1754, Application US/08435628
 ; Patent No. 5817796
 ; GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Drapir, Kenneth
 APPLICANT: McSwiggen, James
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZIMES
 NUMBER OF SEQUENCES: 2627
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 513 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/435, 628
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/373, 124
 FILING DATE: January 13, 1995
 APPLICATION NUMBER: 08/245, 466
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 08/192, 943
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: 07/987, 132
 FILING DATE: December 7, 1992
 APPLICATION NUMBER: 07/936, 422

Query Match Best Local Similarity 91.2%; Score 29.2; DB 1; Length 38; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 US-09-371-772B-8707
 ; Sequence 8707, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan

Query Match Best Local Similarity 91.2%; Score 29.2; DB 1; Length 38; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 US-09-371-772B-8707
 ; Sequence 8707, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00_876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1996-01-08
 PRIOR APPLICATION NUMBER: US 08/584,040
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 8707
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-371-772B-8707
 Query Match 76.8%; Score 29.2; DB 4; Length 38;
 Best Local Similarity 91.2%; Pred. No. 0.00042; Mismatches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 GCAAUUAGGCGGTAGCCGAAATCAG 37
 Db 4 GCAUUCGAAGGCCGUAAGCCGAAAUAGGAG 37
 RESULT 27
 Sequence 9621, Application US/09371772B
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00_876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9621
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-371-772B-9621
 Query Match 76.8%; Score 29.2; DB 4; Length 38;
 Best Local Similarity 91.2%; Pred. No. 0.00042; Mismatches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 CAAUCUGAAGGCCGTAGCCGAAAUACGG 38
 Db 5 CAGUCUTGAAGGCCGTAGCCGAAAUUCAGG 38
 RESULT 28
 Sequence 8786, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: McSwiggen, Jim
 APPLICANT: Pavco, Pam
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00_876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 10855
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-371-772B-10855
 Query Match 76.3%; Score 29; DB 4; Length 38;
 Best Local Similarity 86.5%; Pred. No. 0.00052; Mismatches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CCUGCAUUCUGAAGGCCGTAGCCGAAAUACAG 37
 Db 1 CTUGAGAUUCUGAAGGCCGTAGCCGAAAUACUG 37
 RESULT 30
 Sequence 13264, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.

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; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MEBH00_876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 12264
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; OTHER INFORMATION: n stands for inosine

RESULT 31
US-09-371-772B-7533
; Sequence 7533, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MEBH00_876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8047
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; OTHER INFORMATION: n stands for inosine
; OTHER INFORMATION: n stands for inosine

RESULT 32
US-09-371-772B-8047
; Sequence 8047, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MEBH00_876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8328
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; OTHER INFORMATION: n stands for inosine
; OTHER INFORMATION: n stands for inosine

RESULT 33
US-09-371-772B-8328
; Sequence 8328, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MEBH00_876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8328
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; OTHER INFORMATION: n stands for inosine
; OTHER INFORMATION: n stands for inosine

```

Qy 1 CCGCAUCUGAGGAGCCGUAGGCGGAAA 32
 Db 1 ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 34
 US-09-371-772B-10400
 ; Sequence 10400, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00_876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIORITY FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 10400
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-10400

Query Match 75.8%; Score 28.8; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00064; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Gaps 0;

Qy 3 UGCAAAUCUGAGGGCGGUAGGCCGAAAU 34
 Db 3 UGACAUUCUGAGGGCGGUAGGCCGAAAU 34

RESULT 35
 US-09-371-772B-10648
 ; Sequence 10648, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00_876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIORITY FILING DATE: 1995-10-26
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 10648
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-10648

Query Match 75.8%; Score 28.8; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00064; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Gaps 0;

Qy 3 UGCAAAUCUGAGGGCGGUAGGCCGAAAU 34
 Db 3 UGACAUUCUGAGGGCGGUAGGCCGAAAU 34

RESULT 36
 US-09-371-772B-11044
 ; Sequence 11044, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00_876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIORITY FILING DATE: 1995-10-26
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 11044
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-11044

Query Match 75.8%; Score 28.8; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00064; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Gaps 0;

Qy 6 AAUCGAUAGGCCGTTAAGGCCGAAAUAGC 37
 Db 6 AUUCGAUAGGCCGTTAAGGCCGAAAUAGC 37

RESULT 37
 US-09-371-772B-12223
 ; Sequence 12223, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00_876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIORITY FILING DATE: 1995-10-26
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 12223
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-12223

Query Match 75.8%; Score 28.8; DB 4; Length 38;
 Best Local Similarity 93.8%; Pred. No. 0.00064; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Gaps 0;

Qy 6 AAUCGAUAGGCCGTTAAGGCCGAAAUAGC 37
 Db 6 AUUCGAUAGGCCGTTAAGGCCGAAAUAGC 37

NAME/KEY: misc_feature
; LOCATION: (31).:(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-12223

Query Match ; Best Local Similarity 90.9%; Score 28.8; DB 4; Length 38; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CUGCAUCATGAGCCGUUAGCCGAAAU 34
; Db 2 CUGAAUACUGAUGGCGGUAGCCGAANCAU 34

RESULT 38
US-09-371-772B-12495
; Sequence 12495, Application US/0931772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00_876-J (23/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIO FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12495
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: Enzymatic Nucleic Acid
NAME/KEY: misc_feature
LOCATION: (31).:(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-12495

Query Match ; Best Local Similarity 90.9%; Score 28.8; DB 4; Length 38; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AUUCUGAUGAGCGGUUAGCCGAAUACAG 38
; Db 6 AUUCUGAUGAGCGGUUAGCCGAAUACAG 38

RESULT 40
US-09-371-772B-7626
; Sequence 7626, Application US/0931772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00_876-J (23/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7626
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: Enzymatic Nucleic Acid
NAME/KEY: misc_feature
LOCATION: (31).:(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-7626

Query Match ; Best Local Similarity 90.9%; Score 28.8; DB 4; Length 38; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAUCUGAUGAGCGGUUAGCCGAAUACAG 38
; Db 6 AAUCUGAUGAGCGGUUAGCCGAAUACAG 38

RESULT 39
US-09-371-772B-13894
; Sequence 13894, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00_876-J (23/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26

Search completed: May 13, 2005, 18:27:24
Job time : 94.9636 Secs

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Run on: May 13, 2005, 16:54:55 : Search time 324.036 Seconds
(without alignments)
717.723 Million cell updates/sec

Title: US-09-927-046-2332
Perfect score: 38
Sequence: 1 ccugcaaucugauagggccguuaggccgaaaaucagg 38

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues
Total number of hits satisfying chosen parameters: 5530346

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA:*

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2:	/cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
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11:	/cgn2_6/prodata/2/pubpna/us09c_PUBCOMB.seq:*
12:	/cgn2_6/prodata/2/pubpna/us09c_NEW_PUB.seq:*
13:	/cgn2_6/prodata/2/pubpna/us10_PUBCOMB.seq:*
14:	/cgn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*
15:	/cgn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*
16:	/cgn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*
17:	/cgn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*
18:	/cgn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*
19:	/cgn2_6/prodata/2/pubpna/us10c_NEW_PUB.seq:*
20:	/cgn2_6/prodata/2/pubpna/us11c_NEW_PUB.seq:*
21:	/cgn2_6/prodata/2/pubpna/us60c_NEW_PUB.seq:*
22:	/cgn2_6/prodata/2/pubpna/us60c_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	38	100.0	38	Sequence 2332, AP
2	36	94.7	37	Sequence 5432, AP
3	31.8	83.7	38	Sequence 5304, AP
4	31.8	83.7	38	Sequence 4217, AP
5	31.4	82.6	38	Sequence 3244, AP
6	31.4	82.6	38	Sequence 2304, AP
7	31.4	82.6	38	Sequence 2077-046-2332
8	31.4	82.6	38	Sequence 1796, AP
9	31.4	82.6	38	Sequence 10-09-972-818-954
10	31.4	82.6	38	Sequence 3795, AP
11	31.2	82.1	38	Sequence 8687, AP

RESULT 4
 Qy 2 CGGCAUCUGAGAGCCGTTAGGCCGAAAUCA 36
 Db 2 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CUUUACUAGAGCCGUAGGCCGA 36

GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Invention: Levels of Epidermal Growth Factor Receptors
 / FILE REFERENCE: MBHB00-959-1 (400/018)
 / CURRENT APPLICATION NUMBER: US/09/848,754A
 / CURRENT FILING DATE: 2001-05-03
 / NUMBER OF SEQ ID NOS: 9645
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 4217
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-4217

Query Match	Score	DB	Length	Start	End	Strand
Best Local Similarity	83 %	10	38	0	38	+
Matches	94 3%	Pred.	No.	0.00035		
Qy	2	CUGCAUCUGAGAGCCGTTAGGCCGAAAUCA	36			
Db	2	CUCCAUCAUCUGAGAGCCGUAGGCCGA 36				

RESULT 5
 US-09-800-533A-3244
 / Sequence 3244, Application US/09780533A
 / Publication No. US20030060011A1
 / GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / APPLICANT: Blatt, Larry
 / APPLICANT: McSwiggen, Jim
 / APPLICANT: Chovrila, Bharat
 / APPLICANT: Hieberl, Peter
 / TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 / FILE REFERENCE: MBHB00, 87-A (400/011)
 / CURRENT APPLICATION NUMBER: US/09/780,533A
 / CURRENT FILING DATE: 2001-02-09
 / PRIORITY NUMBER: US 60/181,797
 / PRIORITY FILING DATE: 2000-03-11
 / NUMBER OF SEQ ID NOS: 6679
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 3244
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-800-533A-3244

Query Match	Score	DB	Length	Start	End	Strand
Best Local Similarity	83 %	10	38	0	38	+
Matches	94 3%	Pred.	No.	0.00035		
Qy	3	UGCAUCUGAGAGCCGTTAGGCCGAAAUAC	35			
Db	3	UGAACAUUCUGAGAGCCGUAGGCCGA 35				

RESULT 6
 US-09-827-046-2304
 / Sequence 3796, Application US/09877478
 / Publication No. US20030068301A1
 / GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / APPLICANT: Draper, Kenneth
 / APPLICANT: Blatt, Larry
 / APPLICANT: McSwiggen, Jim
 / APPLICANT: Morrissey, Dave
 / TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 / FILE REFERENCE: MBHB00-845-H (400/029)
 / CURRENT APPLICATION NUMBER: US/09/877,478
 / CURRENT FILING DATE: 2001-12-31
 / PRIORITY NUMBER: US 07/882,712
 / PRIOR FILING DATE: 1992-05-14
 / PRIOR APPLICATION NUMBER: US 09/531,025
 / PRIOR FILING DATE: 2000-03-20
 / PRIOR APPLICATION NUMBER: US 09/636,385
 / PRIOR FILING DATE: 2000-08-09
 / PRIOR APPLICATION NUMBER: US 09/695,347
 / PRIOR FILING DATE: 2000-10-24
 / PRIOR APPLICATION NUMBER: US 08/193,627
 / PRIOR FILING DATE: 1994-02-07
 / PRIOR APPLICATION NUMBER: US 08/433,993
 / PRIOR FILING DATE: 1995-05-04
 / PRIOR APPLICATION NUMBER: US 08/434,504
 / PRIOR FILING DATE: 1995-05-04
 / PRIOR APPLICATION NUMBER: US 09/436,430
 / PRIOR FILING DATE: 1999-11-08
 / NUMBER OF SEQ ID NOS: 6586
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 3796
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-827-046-2304

Query Match	Score	DB	Length	Start	End	Strand
Best Local Similarity	82.6 %	10	38	0	38	+
Matches	97.0%	Pred.	No.	0.00053		
Qy	5	CAUUCUGAGGGCCGUAGGCCGA 37				
Db	5	CAAUCUGAGGGCCGUAGGCCGA 37				

RESULT 7
 US-09-827-478-3796
 / Sequence 3796, Application US/09877478
 / Publication No. US20030068301A1
 / GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / APPLICANT: Draper, Kenneth
 / APPLICANT: Blatt, Larry
 / APPLICANT: McSwiggen, Jim
 / APPLICANT: Morrissey, Dave
 / TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 / FILE REFERENCE: MBHB00-845-H (400/029)
 / CURRENT APPLICATION NUMBER: US/09/877,478
 / CURRENT FILING DATE: 2001-12-31
 / PRIORITY NUMBER: US 07/882,712
 / PRIOR FILING DATE: 1992-05-14
 / PRIOR APPLICATION NUMBER: US 09/531,025
 / PRIOR FILING DATE: 2000-03-20
 / PRIOR APPLICATION NUMBER: US 09/636,385
 / PRIOR FILING DATE: 2000-08-09
 / PRIOR APPLICATION NUMBER: US 09/695,347
 / PRIOR FILING DATE: 2000-10-24
 / PRIOR APPLICATION NUMBER: US 08/193,627
 / PRIOR FILING DATE: 1994-02-07
 / PRIOR APPLICATION NUMBER: US 08/433,993
 / PRIOR FILING DATE: 1995-05-04
 / PRIOR APPLICATION NUMBER: US 08/434,504
 / PRIOR FILING DATE: 1995-05-04
 / PRIOR APPLICATION NUMBER: US 09/436,430
 / PRIOR FILING DATE: 1999-11-08
 / NUMBER OF SEQ ID NOS: 6586
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 3796
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-827-478-3796

LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; US-09-927-046-2332

Query Match 82.6%; Score 31.4; DB 10; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00053; Mismatches 2; Indels 0; Gaps 0;
Matches 32; Conservative 0; Seq ID No. 3196

Qy 1 CCGGCAACUGAUGAGGCCGUTAGGCCGAAAU 34
Db 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAAU 34

RESULT 8

US-09-792-818-954

; Sequence 954, Application US/097922818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlton, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/097922818
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO. 954
; LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-792-818-954

Query Match 82.6%; Score 31.4; DB 10; Length 38;
Best Local Similarity 97.0%; Pred. No. 0.00053; Mismatches 1; Indels 0; Gaps 0;
Matches 32; Conservative 0; Seq ID No. 954
Length: 38

Qy 4 GCGAUCUGAAGCCGUGUAGGCCGAAAUCA 36
Db 4 GCAGCUCGAUGAGGCCGUAGCCGAAAUCA 36

RESULT 9

US-10-342-902-3796

Query Match 82.6%; Score 31.4; DB 17; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00053; Mismatches 2; Indels 0; Gaps 0;
Matches 32; Conservative 0; Seq ID No. 956
Length: 38

Qy 1 CCGGCAACUGAUGAGGCCGUTAGGCCGAAAU 34
Db 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAAU 34

RESULT 10

US-10-669-841-8687

; Sequence 8687, Application US/10669841
; Publication No. US2004012446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macelak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/295,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1607
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8687
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 FEATURE: misc_feature
 LOCATION: (31) - (31)
 OTHER INFORMATION: n stands for inosine
 ;US-10-669-841-8687

Query Match 82.6%; Score 31.4; DB 18; Length 38;
 Best Local Similarity 94.1%; Pred. No. 0.00053; Indels 0; Gaps 0;
 Mismatches 2; Matches 32;

Qy 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAAU 34
 Db 1 CCCGCACACUGAUGAGGCCGUTAGGCCGAAAGUCA 34

RESULT 11
 US-10-138-674-11175
 Sequence 1115, Application US/10138674
 Publication No. US20040077565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138 674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ;US-10-138-674-11175

Query Match 82.1%; Score 31.2; DB 17; Length 38;
 Best Local Similarity 91.7%; Pred. No. 0.00065; Indels 0; Gaps 0;
 Mismatches 33; Conservative 0; Mismatches 3; Matches 33;

Qy 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAUA 36
 Db 1 CCCGCACACUGAUGAGGCCGUTAGGCCGAAAGCA 36

RESULT 12
 US-10-138-674-11662
 Sequence 11662, Application US/10138674
 Publication No. US20040077565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Jaime
 APPLICANT: Bacsoedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138 674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ;US-10-138-674-11662

Query Match 82.1%; Score 31.2; DB 18; Length 38;
 Best Local Similarity 91.7%; Pred. No. 0.00065; Indels 0; Gaps 0;
 Mismatches 33; Conservative 0; Mismatches 3; Matches 33;

Qy 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAAUCA 36
 Db 1 CCCGCACACUGAUGAGGCCGUTAGGCCGAAAGUCA 36

RESULT 13
 US-10-287-949A-11175
 Sequence 1115, Application US/10287949A
 Publication No. US20040102389A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/287,949A
 CURRENT FILING DATE: 2003-04-11
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 11175
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ;US-10-287-949A-11175

Query Match 82.1%; Score 31.2; DB 18; Length 38;
 Best Local Similarity 91.7%; Pred. No. 0.00065; Indels 0; Gaps 0;
 Mismatches 33; Conservative 0; Mismatches 3; Matches 33;

Qy 1 CCUGCAACUGAUGAGGCCGUTAGGCCGAAAUCA 36
 Db 1 CCCGCACACUGAUGAGGCCGUTAGGCCGAAAGUCA 36

RESULT 14
 US-10-287-949A-11662
 Sequence 11662, Application US/10287949A
 Publication No. US20040102389A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Bacsoedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/287,949A
 CURRENT FILING DATE: 2003-04-11
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 11662
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ;US-10-287-949A-11662

Query Match 82.1%; Score 31.2; DB 18; Length 38;
 Best Local Similarity 91.7%; Pred. No. 0.00065; Indels 0; Gaps 0;
 Mismatches 33; Conservative 0; Mismatches 3; Matches 33;

Qy 1 CCUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 36
Db 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| US-10-138-674-9749
; Sequence 9749, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 9749
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-138-674-9749

Query Match 81.1%; Score 30.8; DB 17; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098; Mismatches 0; Indels 0; Gaps 0;
Matches 32; Conservative 0; MisMatch 2;

Qy 2 CUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 35
Db 2 CGCGACUGCAGAUGAGGCCGUUAGGCCGAAAUCA 35

RESULT 16
US-10-138-674-10950
; Sequence 10950, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 10950
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-138-674-10950

Query Match 81.1%; Score 30.8; DB 17; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098; Mismatches 0; Indels 0; Gaps 0;
Matches 32; Conservative 0; MisMatch 2;

Qy 1 CCUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 34
Db 1 CCUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 34

RESULT 17
US-10-287-949A-9749
; Sequence 9749, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 9749
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-287-949A-9749

Query Match 81.1%; Score 30.8; DB 18; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098; Mismatches 0; Indels 0; Gaps 0;
Matches 32; Conservative 0; MisMatch 2;

Qy 1 CCUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 34
Db 1 CCUGCAUCUGAUGAGCCGTTAGGCCGAAAUCA 34

RESULT 19
US-09-848-754A-5340
; Sequence 5340, Application US/09848754A
; Publication No. US20030073207A1

GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Tissue Regeneration
 TITER OR INVENTION: Levels of Epidermal Growth Factor Receptors
 FILE REFERENCE: MBH00-958-I (400/018)
 CURRENT APPLICATION NUMBER: US/09/848,754A
 CURRENT FILING DATE: 2001-05-03
 NUMBER OF SEQ ID NOS: 9645
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 5340
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
 NAME/KEY: misc_feature
 LOCATION: (31)..(31)
 OTHER INFORMATION: n stands for inosine
 US-09-848-754A-5340

Query Match 80.5%; Score 30.6; DB 10; Length 38;
 Best Local Similarity 86.8%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 33; Conservative 0; Mismatches 5; Length 38;
 Qy 1 CCUGCAUCUAGGAGGCCGTUAGCCGAAGAACGG 38
 Db 1 CCUGCUGUGAGGAGGCCGTUAGCCGAAGAACGG 38

RESULT 20
 Sequence 1007, Application US/10156306
 Publication No. US20030115017A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: McCwiggan, James
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Tissue Regeneration
 FILE REFERENCE: MBH01-664-A (400/050)
 CURRENT APPLICATION NUMBER: US/10/156,306
 CURRENT FILING DATE: 2003-05-28
 NUMBER OF SEQ ID NOS: 8013
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1007
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial sequence: Enzymatic Nucleic Acid
 US-10-156-306-1007

Query Match 80.5%; Score 30.6; DB 15; Length 38;
 Best Local Similarity 89.2%; Pred. No. 0.0012; Indels 4; Gaps 0;
 Matches 33; Conservative 0; Mismatches 4; Length 38;
 Qy 1 CCUCCAUCUAGGAGGCCGTUAGCCGAAGAACGG 37
 Db 1 CUUGCGAACUGAGGAGGCCGTUAGCCGAAGAACGG 37

RESULT 21
 Sequence 11851, Application US/10138674
 Publication No. US2004007565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: Mcswiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Tissue Regeneration
 FILE REFERENCE: MBH00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/287,949A
 CURRENT FILING DATE: 2003-04-11
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 11851
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-10-138-674-11851

Query Match 80.5%; Score 30.6; DB 18; Length 38;
 Best Local Similarity 89.2%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 33; Conservative 0; Mismatches 4; Length 38;
 Qy 2 CUGCAUCUAGGAGGCCGTUAGCCGAAGAACGG 38
 Db 2 CUCCKAUUCUGAGGAGGCCGTUAGCCGAAGAACGG 38

RESULT 23
 Sequence 3295, Application US/09780533A
 Publication No. US20030060611A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 APPLICANT: Chowkira, Bharat
 APPLICANT: Haebeli, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Nogo Gene
 FILE REFERENCE: MBH00-878-A (400/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,797
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: PatentIn version 3.0

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; SEQ ID NO: 3395
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-780-533A-3395

Query Match Similarity 80.0%; Score 30.4; DB 10; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.0015; Pred. No. 0.0015; 1; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CAUUCUGAAGGCCGUTAGCCGAAAUCA 36
Db      5 CAAACUGAAGGCCGUTAGCCGAAAUCA 36

RESULT 24
US-09-780-533A-3392
; Sequence 3392, Application US/09780533A
; Publication No. US2003006061AI
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowkira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00-878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3392
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; US-09-780-533A-3392

Query Match Similarity 80.0%; Score 30.4; DB 10; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0015; 2; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CGUCGAUCUGAAGGCCGUTAGCCGAAAUCA 34
Db      2 CGUCGAACUGAAGGCCGUTAGCCGAAAUCA 34

RESULT 25
US-09-848-754A-4314
; Sequence 4314, Application US/09848754A
; Publication No. US2003007320A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Human Disease
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptor
; FILE REFERENCE: MBHB00-950-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4314
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-848-754A-4314

Query Match Similarity 80.0%; Score 30.4; DB 17; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.0015; Pred. No. 0.0015; 1; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 AUCUGAAGGCCGUTAGCCGAAAUCA 38
Db      7 AUGCUGAAGGCCGUTAGCCGAAAUCA 38

RESULT 26
US-09-780-164-1164
; Sequence 1164, Application US/09780164A
; Publication No. US2003009246A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1164
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-780-164-1164

Query Match Similarity 80.0%; Score 30.4; DB 10; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.0015; 1; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CAUUCUGAAGGCCGUTAGCCGAAAUCA 36
Db      5 CAAUCUGAAGGCCGUTAGCCGAAAUCA 36

RESULT 27
US-10-138-674-11690
; Sequence 11690, Application US/10138674A
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Human Disease
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20022
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11690
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-138-674-11690

Query Match Similarity 80.0%; Score 30.4; DB 17; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.0015; Pred. No. 0.0015; 1; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCUGCAUCUGAUGAGCCGUNAGGCCGAA 32
 Db 1 CCGCAAGCUGAUGCAGGCCGUNAGGCCGAA 32

RESULT 28
 US-10-138-674-12840
 ; Sequence 12840, Application US/10138674
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/138,674
 ; CURRENT FILING DATE: 2002-05-03
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12840
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

QY 7 AUCUGAUGAGGCCGUUAGGCCGAAAUACAGG 38
 Db 7 ACCUGAUGAGGCCGUUAGGCCGAAAUACAGG 38

RESULT 29
 US-10-287-949A-11690
 ; Sequence 11690, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11690
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

QY 1 CCUGCAUCUGAUGAGCCGUNAGGCCGAA 32
 Db 1 CCGCAAGCUGAUGCAGGCCGUNAGGCCGAA 32

RESULT 30
 US-10-287-949A-12840
 ; Sequence 12840, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12840
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

QY 7 AUCUGAUGAGGCCGUUAGGCCGAAAUACAGG 38
 Db 7 ACCUGAUGAGGCCGUUAGGCCGAAAUACAGG 38

RESULT 31
 US-09-780-533A-3424
 ; Sequence 3424, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowria, Bharat
 ; APPLICANT: Haeborli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBHB00-878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3424
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

QY 2 CUGCAUCUGAUGAGCCGUNAGGCCGAAUACA 36
 Db 2 CUGCAUCUGAUGAGCCGUNAGGCCGAAUACA 36

RESULT 32
 US-10-138-674-10420
 ; Sequence 10420, Application US/10138674

Publication No. US20040077563A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBHB00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138,674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 10420
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-10-138-674-10420
 Query Match 79.5%; Score 30.2; DB 17; Length 38;
 Best Local Similarity 91.4%; Pred. No. 0.0018;
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 CGGCAUUCUGAGGAGCCGUUAGGCCAAAUCA 36
 Db 2 CUACAGCUGAGGAGCCGUUAGGCCAAAUCA 36

RESULT 33
 US-10-287-949A-10420
 ; Sequence 10420, Application US/10287949A
 ; Publication No. US2004010289A1
 ; GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / APPLICANT: Pavco, Pam
 / APPLICANT: McSwiggen, Jim
 / APPLICANT: Stinchcomb, Dan
 / APPLICANT: Escobedo, Jaime
 / TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Vascular Endothelial Growth Factor Receptor
 / FILE REFERENCE: MBHB00-876-N (400/049)
 / CURRENT APPLICATION NUMBER: US/10/287,949A
 / CURRENT FILING DATE: 2003-04-11
 / NUMBER OF SEQ ID NOS: 20822
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 10420
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 / US-10-287-949A-10420
 Query Match 79.5%; Score 30.2; DB 18; Length 38;
 Best Local Similarity 91.4%; Pred. No. 0.0018;
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 CGGCAUUCUGAGGAGCCGUUAGGCCAAAUCA 36
 Db 2 CUACAGCUGAGGAGCCGUUAGGCCAAAUCA 36

RESULT 34
 US-09-927-046-2560
 ; Sequence 2560, Application US/09927046
 ; Publication No. US2003006946A1
 ; GENERAL INFORMATION:
 / APPLICANT: Ribozyme Pharmaceuticals, Inc.
 / APPLICANT: McSwiggen, Jim
 / APPLICANT: Thompson, Jim
 / APPLICANT: Ayers, Dave
 / APPLICANT: Grube, Andrew
 / APPLICANT: Szymkowski, Edmund
 / TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric Channel-1
 / FILE REFERENCE: 249/021
 / CURRENT APPLICATION NUMBER: US/09/927,046
 / CURRENT FILING DATE: 2001-08-09
 / NUMBER OF SEQ ID NOS: 5450
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 2560
 / LENGTH: 38
 / TYPE: RNA
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 / US-09-927-046-2560
 Query Match 78.9%; Score 30; DB 10; Length 38;
 Best Local Similarity 86.8%; Pred. No. 0.0022;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CCUGCAUUCUGAGGAGCCGUUAGGCCAAAUCAAGG 38

Db 1 ||||| CCCAACAGCUGAUGAGCCGUAGGCGGAAGAUGAGG 38
; Sequence 4081, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relating to Levels of Epileptic Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 4081
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-848-754A-4081
; Query Match 78.9%; Score 30; DB 10; Length 38;
; Best Local Similarity 86.8%; Pred. No. 0.0022; Mismatches 5; Indels 0; Gaps 0;
; Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
; Qy 1 CCUGCAUCUGAUGAGCCGUAGGCCGAAAAAUCAGG 38
; Db 1 CCUCCAGCUGAUGAGCCGUAGGCCGAAAGUCAUG 38
; RESULT 37
; sequence 1268, Application US/09716474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Booher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattayey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 1268
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-776-474-1268
; Query Match 78.9%; Score 30; DB 10; Length 38;
; Best Local Similarity 86.8%; Pred. No. 0.0022; Mismatches 5; Indels 0; Gaps 0;
; Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
; Qy 1 CCUGCAUCUGAUGAGCCGUAGGCCGAAAAAUCAGG 38
; Db 1 CCUCCAGCUGAUGAGCCGUAGGCCGAAAGUCAUG 38
; RESULT 38
; sequence 814, Application US/10156305
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 814
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-156-306-814
; Query Match 78.9%; Score 30; DB 15; Length 38;
; Best Local Similarity 100.0%; Pred. No. 0.0022; Mismatches 0; Indels 0; Gaps 0;
; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 6 AAUCUGAUGAGCCGUAGGCCGAAAUAC 35
; Db 6 AAUCUGAUGAGCCGUAGGCCGAAAUAC 35
; RESULT 39
; sequence 4583, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relating to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 4583
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-10-156-306-4583
; Query Match 78.9%; Score 30; DB 15; Length 38;
; Best Local Similarity 86.8%; Pred. No. 0.0022; Mismatches 5; Indels 0; Gaps 0;
; Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
; Qy 1 CCUGCAUCUGAUGAGCCGUAGGCCGAAAAAUCAGG 38
; Db 1 CCUCCAGCUGAUGAGCCGUAGGCCGAAAGUCAUG 38
; RESULT 40
; sequence 2631, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirona Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; RESULT 38
; US-10-156-306-814

CURRENT FILING DATE: 2003-01-15
 PRIOR APPLICATION NUMBER: US 09/877,478
 PRIOR FILING DATE: 2003-06-08
 PRIOR APPLICATION NUMBER: US 09/531,025
 PRIOR APPLICATION NUMBER: US 09/636,385
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: US 09/696,347
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 08/193,527
 PRIOR FILING DATE: 1994-02-07
 PRIOR APPLICATION NUMBER: US 07/882,712
 PRIOR FILING DATE: 1992-05-14
 PRIOR APPLICATION NUMBER: US 09/436,430
 PRIOR FILING DATE: 1999-11-08
 NUMBER OF SEQ ID NOS: 6592
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 2631
 LENGTH: 38
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-10-342-902-2631

Query Match 78.9%; Score 30; DB 17; Length 38;
 Best Local Similarity 86.8%; Pred. No. 0.0022;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CCUGCAUCUGAAGGCCGUAGCCGAAAUUCAGG 38
 Db 1 CCAAACAGCTUGAUGAGGCCGUTAGGCCGAAGAUAGGG 38

Search completed: May 13, 2005, 18:25:02

Job time : 326.036 secs

FEATURES		source	FEATURES	source
Source				
1. (bases 1 to 92)			1. .94	
Walbot, V.			/organism="Mus musculus"	
Unpublished (2001)			/mol_type="genomic DNA"	
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			/strain="C57BL/6J"	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			/db_xref="Taxon:10090"	
clade; Panicoideae; Andropogoneae; Zea.			/clone="UDGC2M070F19"	
Class: transposon-tagged.			/sex="Male"	
Location/Qualifiers			/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-	
			/clone lib="Mouse 10kb plasmid UDGCIM library"	
			/note="Vector: PWP-2nv; Purified genomic DNA from M.	
			musculus C57BL/6J (male)" was obtained from the Jackson	
			Laboratory Mouse DNA Resource	
			(http://www.jax.org/resources/documents/dnare/)	
			The DNA was hydrodynamically sheared by repeated passage through a	
			0.005 inch orifice at constant velocity. The sheared DNA	
			was blunt end-repaired with T4 DNA polymerase and T4	
			polynucleotide kinase. Adaptor oligonucleotides were	
			ligated to the blunt ends in high molar excess. The	
			adapted DNA was purified and size-selected for a 9.5 to	
			10.5 kb range using preparative agarose gel	
			electrophoresis. Vector DNA was prepared from a derivative	
			of pWD42 (gi 472114 gb AF129072.1)	
			, a copy-number inducible derivative of plasmid R1. The vector was ligated	
			with adaptors complementary to the insert adaptors and	
			purified. The sheared, adapted mouse DNA was annealed to	
			adapted vector DNA, and transformed into	
			chemically-competent E. coli XL10-Gold (Stratagene) cells	
			and selected for ampicillin resistance."	
ORIGIN			RESULTS	
Query Match	44.7%	Score 17; DB 8; Length 92;	RESULT 6	
Best Local Similarity	57.6%	Pred. No. 1.5e+04; Matches 19; Conservative 4; Mismatches 10; Indels 0; Gaps 0;	Query	1 CCUGCAUCUGAAGGCCGUAGGCCGAA 33
QY			Db	57 CCTGCACTGATGAGGTGGTGGAGA 89
KEYWORDS				
SOURCE				
ORGANISM	Mus musculus (house mouse)			
RESULT 7			RESULTS	
REFERENCE	1 (bases 1 to 94)		RESULT 7	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meeney, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederauer, A., and Wright, D., Weiss, R.		Query	1 AU105965
ACCESSTION	AZ807494		Match	5 CAUCAUGAGGCGCCUUAAGCCGAAAUACAG 37
VERSION	AZ807494.1		Db	88 CGTCGATGAGGCCGAAGTCGCCCATCAG 56
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 50)			
AUTHORS	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sase, J., Hata, H., Ora, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Shiyama, A. and Sugano, S.			
TITLE	Diverse transcriptional initiation revealed by fine, large-scale			

		JOURNAL	Biotechniques	35 (6), 1164-1168 (2003)
REFERENCE		PUBLISHED	14/08/2005	
AUTHORS		REFERENCE	4 (bases 1 to 67)	
TITLE		AUTHORS	Li, Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.	
JOURNAL		COMMENT	Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany	
MEDLINE			This sequence has been recovered from the left border of the T-DNA.	
PUBMED			It indicates an insertion close to or within gene At1g55130.	
COMMENT			Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.	
FEATURES	Source		'GABI', Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/Gabi-Kat/ .	
		FEATURES	Location/Qualifiers	
			1. .91	
			/organism="Arabidopsis thaliana"	
			/mol_type="mRNA"	
			/ecotype="Columbia"	
			/db_xref="taxon:3702"	
			/clone="PAZNT10502R"	
			/tissue="liquid-cultured seedlings"	
			/clone_lib="Arabidopsis thaliana liquid-cultured seedlings	
			/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:	
			XbaI"	
			ORIGIN	
			Query Match	43.7%; Score 16.6; DB 1; Length 91;
			Best Local Similarity	51.6%; Pred. No. 2.3e-04; Mismatches 16; Conservative 6; Indels 0; Gaps 0;
			Matches	
Qy	3 ucgcacuucugacggccggcgugccaaaa 33	Qy	4 GCAAUUCUGAGGCCGGUAGGCCGAAAUACAG 37	
Db	91 TCGAATTTGTTGCAACCGTTAGGTGAAA 61	Db	14 GAAACCGATTTGAGCCGGTTAGCACGAAACGAG 47	
			RESULT 11	
LOCUS	BX655236	DEFINITION	Arabidopsis thaliana T-DNA flanking sequence	
ACCESSION	BX655236	VERSION	67 bp	DNA
VERSION	BX655236.1	KEYWORDS	linear	GSS
SOURCE	Arabidopsis thaliana (thale cress)	ORGANISM		
			RESULT 12	
			Query Match	43.2%; Score 16.4; DB 9; Length 67;
			Best Local Similarity	58.8%; Pred. No. 2.7e-04; Mismatches 20; Conservative 3; Indels 0; Gaps 0;
			Matches	
Qy	4 GCAAUUCUGAGGCCGGUAGGCCGAAAUACAG 37	Qy	1 GAAACCGATTTGAGCCGGTTAGCACGAAACGAG 47	
Db	14 GAAACCGATTTGAGCCGGTTAGCACGAAACGAG 47	Db		
			RESULT 13	
LOCUS	CN165896/c	DEFINITION	Arabidopsis thaliana T-DNA flanking sequence	
ACCESSION	CN165896	VERSION	100 bp	mRNA
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Arabidopsis.	ORGANISM	linear	EST
SOURCE				02-APR-2004
REFERENCE				
AUTHORS	Li,Y., Rosso,M.G., Strizhov,N., Vithoever,P. and Weisshaar,B.	REFERENCE		
TITLE	GABI-Kat SimpleSearch: a flankin sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana	AUTHORS	Smith,T.P.L., Freking,B.A., Ford,J.J., Villet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keke,J.W.	
JOURNAL	Bioinformatics	TITLE	Porcine EST Collection using a normalized library constructed from embryos representing early developmental stages	
MEDLINE	1441-1442 (2003)	COMMENT	Unpublished (2003)	
PUBMED	22755829	CONTACT	Contact: Smith TPL	
REFERENCE	12874060	ADDRESS	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA	
AUTHORS	Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.	TEL	Tel: 402 752 4366	
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics	FAX	Fax: 402 752 4390	
JOURNAL	Plant Mol. Biol.	EMAIL	Email: smith@email.marc.usda.gov	
MEDLINE	53 (1-2), 247-259 (2003)		Single pass sequencing: Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.	
PUBMED	2311747	PLATE	Plate: TMW065 row: E column: 17	
REFERENCE	14756321	SEQ PRIMER	Seq primer: TAGAGGCACAGTGAGG	
AUTHORS	Strizhov,N., Li,Y., Rosso,M.G., Vithoever,P., Dekker,K.A. and Weisshaar,B.	LOCATION	Location/Qualifiers	
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines	FEATURES	1..100 /organism="Sus scrofa"	

REFERENCE	2 (bases 1 to 82)	/dev/stage="stage 15" /clone.lib="NIBB Mochii normalized Xenopus neurula library"
AUTHORS	Balzergue, S.	
TITLE	Direct Submission	
JOURNAL		
COMMENT	Gaston Cremer, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of <i>Arabidopsis thaliana</i> plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.verrailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.Genoplante.com and http://genoplante-info.infobiogen.fr).	
FEATURES		
source	Location/Qualifiers	
ORIGIN		
Query Match	42.1%; Score 16; DB 9; Length 91;	
Best Local Similarity	57.6%; Pred. No. 4.2e+04; Mismatches 5; Indels 0; Gaps 0;	
Matches	19; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	
Qy	6 AAUCUGAUGGCCGUAGGCCGAAAUACGG 38	
Db	1 ATATGATTCAGCCCTCAGGAATAAACGG 33	
RESULT 16		
BJ029544	BJ029544 91 bp mRNA linear EST 26-SEP-2003	
LOCUS	XL012m10 5', mRNA sequence.	
DEFINITION	Xenopus laevis CDNA Clone XL012m10 5', mRNA sequence.	
ACCESSION	BJ029544	
VERSION	BJ029544.1	
KEYWORDS	EST	
SOURCE	Xenopus laevis (African clawed frog)	
ORGANISM	Xenopus laevis	
REFERENCE		
COMMENT	The information of this clone is available through the following URL: http://xenopus.nibb.ac.jp .	
FEATURES		
source	Location/Qualifiers	
ORIGIN		
Query Match	42.1%; Score 16; DB 1; Length 94;	
Best Local Similarity	53.1%; Pred. No. 4.2e+04; Mismatches 5; Indels 0; Gaps 0;	
Matches	17; Conservative 5; Mismatches 10; Indels 0; Gaps 0;	
Qy	6 AAUCUGAUGGCCGUAGGCCGAAAUACGG 37	
Db	34 ATATGATTCAGCCCTCAGGAACGATCGG 65	
RESULT 18		
AA237314	AA237314 97 bp mRNA linear EST 03-MAR-1997	
LOCUS	XL012m10 1 Soares mouse NMI Mus musculus cDNA clone IMAGE_6809475	
DEFINITION	similar to TR:GI136414 GI136414 KIA0177 PROTEIN ; mRNA sequence.	
ACCESSION	AA237314	
VERSION	AA237314.1	
KEYWORDS	EST	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

		COMMENT	Contact: Robert B. Weiss University of Utah Genome Center
REFERENCE	1 - (bases 1 to 97)	DEFINITION	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
AUTHORS	Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geibel,S., Kocab,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thaising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	VERSION	Bal1, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu
JOURNAL	Unpublished (1996)	PLATE	Invert Length: 10000 Std Error: 0.00
COMMENT	Contract: Marr,M/Mouse EST Project The WashU-HMM Mouse EST Project WashU-HMM Mouse EST Project	SEQ PRIMER	Plate: 0153 row: C column: 11 Seq primer: CACACGGGAGACGCTATGACC Class: plasmid ends
FEATURES	Location/Qualifiers	High quality sequence stop: 65. Location/Qualifiers	
Source	1. .97 /organism="Mus musculus" /mol_type="mRNA" /db_xref="TAXON:10090" /clone="IMAGE:68047" /tissue_type="Liver" /lab_host="DHIOB" /clone_lib="Soares mouse NML" /note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with Not I - oligo(dT) primer [5', TGTTCCCATCTGAGTGGAGCGGCCGAACTTTTTTTTTTTT 3']; double-stranded DNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."	1. .65 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="TAXON:10090" /clone="NUGCIM0155C11" /sex="Male" /lab_host="E. Coli strain XJU0-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid NUGCIM library" /note="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi:473214 gb AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XJU0-Gold (Stratagene) cells and selected for ampicillin resistance."	
ORIGIN	Query Match Score 42.1%; DB 1; Length 97; Best Local Similarity 58.3%; Pred. No. 4.2e+04; Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;	Query Match Score 41.6%; DB 8; Length 65; Best Local Similarity 59.3%; Pred. No. 4.9e+04; Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	
Qy	6 AAGCTTGTAGGAGCCGCTTGTAGCCGA 29 69 ATTGTGATGAGGACTTTAGCCGA 92	Qy	1 CCGUGAACUGAAGAGGCCGCTTGTAGGCC 27 27 CCTTCCTTCCAGTGAGGCCGATAGGCC 1
Db		Db	
RESULT 19		RESULT 20	
A2391476/c		CAS87380/c	
LOCUS	A2391476 65 bp DNA linear GSS 03-OCT-2000	LOCUS	CAS87380
DEFINITION	IM0153C1R Mouse 10kb plasmid UGCGC library Mus musculus genomic clone UGCGCIM0153C1 R, genomic survey sequence.	DEFINITION	LBRL1P6TP cDNA from mouse aorta Mus musculus genomic
ACCESSION	AV2391476	ACCESSION	CAS87380
VERSION	A2391476.1 GI:1056519	VERSION	CAS87380.1 GI:40792559
KEYWORDS		KEYWORDS	EST
GSS		SOURCE	Mus musculus (house mouse)
SOURCE	Mus musculus (house mouse)	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ORGANISM		REFERENCE	1 (bases 1 to 65)
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	AUTHORS	Borangi,S., Andersson,T., Thelin,A., Odeberg,J. and Lundeberg,J.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.	JOURNAL	Vascular gene expression by representational difference analysis unpublished (2002)
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert	COMMENT	Contact: Andersson Tove Department of Biotechnology Teknikringen 34, Plan 6, 100 44 Stockholm, Sweden
JOURNAL	Unpublished (2000)	KTH	

		Qy	12 AUGAGCCGCGUAGGCCGAAAUACGG 38
		: : : :	76 bp mRNA linear EST 05-DEC-2002
		Db	34 ATGATGCAGTTAGCAGAAATAATGAGG 60
FEATURES	Source		
		RESULT 22	
		CA79314/c	
		LOCUS CA79314	
		DEFINITION Cac BL 3324 Cac BL (Bean and Leaf from Amelonado type Cacao)	
		ACCESSION CA79314	
		VERSION CA79314.1	
		KEYWORDS EST	
		ORGANISM Theobroma cacao (cacao)	
		SOURCE Theobroma cacao	
		COMMENT Theobroma; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicots; core eudicots; Spermatophyta; Magnoliopsida; eucommids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.	
Qy		REFERENCE 1 (bases 1 to 76)	
Db		AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Ratzel, B.R. and Jones, C.A.	
		TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties	
		JOURNAL Planta 216 (2), 255-264 (2002)	
		MEDLINE 22337596	
		PUBMED 12447539	
		COMMENT Contact: Jones, Paul	
		Masterfoods	
		3a Dundee Road, Slough, Berkshire, UK, SL1 4LG	
		TeL: +44 164 416644	
		Email: Paul.Jones@eu.effem.com	
FEATURES	source		
		RESULT 21	
		CD963815	
		LOCUS CD963815	
		DEFINITION SDY106 GeneTag2 Zea mays cDNA, mRNA sequence.	
		ACCESSION CD963815	
		VERSION CD963815.1	
		KEYWORDS EST.	
		SOURCE Zea mays	
		ORGANISM Zea mays	
		REFERENCE 1 (bases 1 to 72)	
		AUTHORS Genoplante.	
		TITLE Genoplante, a major partnership french program in plant genomics	
		JOURNAL Unpublished (2003)	
		COMMENT Contact: Genoplante	
		Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France	
		Tel: 33 1 69 47 54 00	
		Fax: 33 1 69 47 54 10	
		This sequence has been generated in the framework of the french plant genomics programme 'genoplante' (http://www.genoplante.com) and http://genoplante-info.infobiogen.fr .	
FEATURES	Source		
		ORIGIN	
		RESULT 23	
		BG052646/c	
		LOCUS BG052646	
		DEFINITION 1055310-5 NIA Mouse Newborn Kidney cDNA Library2 (Short) Mu	
		ACCESSION BG052646	
		VERSION BG052646.1	
		KEYWORDS EST.	
		SOURCE Mus musculus (house mouse)	
		ORGANISM Mus musculus	
		REFERENCE 1 (bases 1 to 89)	
		AUTHORS Piao, Y., Ko, N.T., Lin, M.K. and Ko, M.S.H.	
ORIGIN			
		Query Match 41.6%; Score 15.8; DB 6; Length 72;	
		Best Local Similarity 59.3%; Pred. No. 5e+04;	
		Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	

TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNA by a universal PCR amplification method
JOURNAL Genome Res. 11. (9), 1553-1558 (2001)
MEDLINE 2142998
PUBMED 11544199
COMMENT Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgaun.grc.nia.nih.gov
URL: http://lgaun.grc.nia.nih.gov/cDNA/cDNA.html
Plate: 10955 row: G column: 10
Seq primer: -21M13 Reverse
High quality sequence stop: 89
POLY=A>No.

FEATURES

Source

Location/Qualifiers

1. .89

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nblast:LG0955G10-5"
/db_xref="taxon:10090"
/clone="LG0955G10"
/tissue_type="Newborn Kidney"
/dev_stage="Newborn"
/lab_host="DHIOB"
/clone_lib="NIA Mouse Newborn Kidney cDNA Library2
(Short)"

Note= "Vector: pSPORT1 (Invitrogen); site_1: Sall; site_2: NotI. Mouse cDNA project by the laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgaun.grc.nia.nih.gov/cDNA). This is a short-ranscript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). In brief, double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen; 5'-
GAATTCCTCTGATGCCGGCGCCCTTTTTTTT-3'] from 26 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker (U-Sal), purified by phenol/chloroform, and separated from free linkers by Centriprep 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-L. The products were purified by phenol/chloroform and Centriprep 100. The cDNAs were digested with Sall and NotI enzymes and cloned into Sall/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 1.5 kb. The library was constructed by Yulan Piao(NIA)."

ORIGIN

Query Match 41.6%; Score 15.8; DB 4; Length 89;
Best Local Similarity 63.0%; Pred. No. 5.1e+04; Matches 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GRUGAGGCCGTTAGGCCGAAACAUACAG 37

Db 67 GTGGGGCTGGTAGGCCAATGATGAG 41

RESULT 24

Query Match 41.6%; Score 15.8; DB 4; Length 89;
Best Local Similarity 63.0%; Pred. No. 5.1e+04; Matches 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GRUGAGGCCGTTAGGCCGAAACAUACAG 37

Db 67 GTGGGGCTGGTAGGCCAATGATGAG 41

REFERENCE

AUTHORS

TITLE Genetrap2: a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplante

Genoplante
93 rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 00

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

Source

Location/Qualifiers

1. .94

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_lib="Genetrap2"

ORIGIN

Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 92)
Zambrowicz, B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., Beltran-de-Rio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
Fridle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlauft,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-4114 (2003)

REFERENCE

AUTHORS

TITLE Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

JOURNAL Lexicon Genetics Incorporated

COMMENT

4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com

FEATURES

source

Location/Qualifiers

1. .92

/organism="Mus musculus"
/mol_type="mRNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OSTR45022"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

RESULT 25

LOCUS CD947628

DEFINITION SAA_70 Genetrap2 Zea mays cDNA, mRNA sequence.

ACCESSION CD947628

VERSION CD947628.1 GI:32795392

KEYWORDS EST.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplanteae; Streptophyta; Embryophyt; Tracheophyta; Spermatophyt; Magnoliophyt; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE Genoplante, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplante

Genoplante
93 rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 00

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

Source

Location/Qualifiers

1. .94

/organism="Zea mays"
/mol_type="mRNA"
/clone_lib="Genetrap2"

ORIGIN

Qy	7	ATCGAAGGAGGCGTGTAGGCCAAAA	33	Query Match Best Local Similarity 66.7%; Pred. No. 5.2e+04; Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;	Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D., Qian, N., Shaw, J. J., Schrick, J. J., Shi, Z.-Z., Sparks, M. J., Van Sligchhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C., and Sands, A. T.
Db	67	ACAGAGGGCCATTAGGAGGAAATA	41	COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP	OmniBank
RESULT	26			JOURNAL Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com	
LOCUS	CV519527	CV519527	94 bp	mrRNA	linear EST 06-OCT-2004
DEFINITION	0089P00302.x0_E02	Mimulus guttatus library 2 Mimulus guttatus cDNA clone 0089P00302.x0_E02,	mRNA sequence.	Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)	Class: Gene Trap
ACCESSION	CV519527	CV519527			
VERSION	CV519527.1	CV519527.1			
KEYWORDS	EST	EST			
SOURCE	Mimulus guttatus (spotted monkey flower)				
ORGANISM	Mimulus guttatus				
REFERENCE					
AUTHORS	Willis,J., Vision,T., Dietrich,F. S. and Allen,A.				
TITLE					
JOURNAL					
COMMENT	Unpublished (2004)				
CONTACT	Contact: Willis J				
DUKE	University				
BIOLOGY	Department of Biology				
TELE	0724A Biological Sciences Science Drive, Durham, NC 27708, USA				
FAX	919 660 7293				
EMAIL	Jwillis@duke.edu				
PLATE	0089P0030	row: 02	column: E		
SEQ_PRIMER	T7				
FEATURES	High quality sequence stop: 667.				
source	Location/Qualifiers				
	1..94				
	/organism="Mimulus guttatus"				
	/mol_type="mRNA"				
	/strain="129sv/Ev"				
	/db_xref="txaxon:4155"				
	/clone="0089P00302.x0_E02"				
	/clone_id="0089P00302.x0_E02"				
	/note="Mimulus guttatus library 2"				
	/note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"				
ORIGIN					
RESULT	28	AZ608536/c	41.6%	Score 15.8; DB 7; Length 94;	Query Match Best Local Similarity 57.1%; Pred. No. 5.2e+04; Matches 20; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
LOCUS	AZ608536	AZ608536			
DEFINITION	0432N13R	0432N13R	97 bp	DNA linear GSS 13-DEC-2000	clone UGGCIM0432N13_R, genomic survey sequence.
ACCESSION	AZ608536	AZ608536			
VERSION	AZ608536.1	AZ608536.1			
KEYWORDS	GSS.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus (house mouse)				
REFERENCE					
AUTHORS	Dunn,D., Royagi,A., Barber,M., Beacons,T., Dval,B., Hamil,C., Islam,H., Longore,S., Mahmoud,M., Meen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.				
COMMENT	Plasmid insert				
JOURNAL	Unpublished (2000)				
CONTACT	Contact: Robert B. Weiss				
UNIVERSITY	University of Utah Genome Center				
UNIVERSITY	University of Utah				
DEFINITION	0511742 Mus musculus 129sv/Ev	0511742	94 bp	mrRNA linear GSS 01-OCT-2003	0511742 Mus musculus 129sv/Ev mrRNA sequence.
LOCUS	CG528153	CG528153			
ACCESSION	CG528153	CG528153			
VERSION	CG528153.1	CG528153.1			
KEYWORDS	GR:37314725				
SOURCE	GSS				
ORGANISM	Mus musculus (house mouse)				
REFERENCE					
AUTHORS	1 (bases 1 to 94); Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, J.J., Beltran, H., Edwards, J., Finch, R.A., Pigott, J., Beltran, H., Buxton, E.C., Edwards, J., Finch, R.A., Fiddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiang, C.,				
FEATURES	High quality sequence stop: 97.				
source	Location/Qualifiers				
	1..97				
	/organism="Mus musculus"				
	/mol_type="Genomic DNA"				
	/strain="C57BL/6J"				

/db_xref="TAXON:10990"
 /clone="UUGGCM0432N13"
 /sex="Male"
 /lab_hsb="E. coli strain XL10-Gold, Tr-resistant, F-"
 /clone_label="Mouse 10kb Plasmid uggcm library"
 /note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnaree/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt-end-repaired with T4 DNA Polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (91|473211|gb|AF129072.1), a copy-number
 inducible derivative of Plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into chemically-competent
 E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."/>

/db_xref="taxon:10090"
/clone="DUGCIM0306308"
/lcl_hos="E. coli strain XL10-Gold, T₁-resistant, F-"
/sex="Male"
/clone_lis="Mous 1.0kb plasmid UGGCM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.Jax.org/resources/documents/dmabs/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T₄ DNA polymerase and T₄
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

DEFINITION	AZ019711	98 bp	DNA	linear	GSS	04-OCT-2000
ACCESSION	IM0306J08R	Mouse	10kb plasmid	UUGC1M0306J08 R,	genomic	
VERSION	AZ481971					
KEYWORDS	AZ481971.1					
SOURCE	GSS.					
ORGANISM	Mus musculus					
Bukata, M.	Metazoa;	Chordata;	Craniate;	Vertebrata;	Euteleostomi;	
Mammalia;	Eutheria;	Rodentia;	Sciurognathi;	Muridae;	Murinae;	Mus.
REFERENCE	1 (bases 1 to 98)					
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beaumont, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss					
	University of Utah Genome Center					
	University of Utah					
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT					
	84112, USA					
	Tel: 801 585 5606					
	Fax: 801 585 7177					
	Email: ddunn@genetics.utah.edu					
	Insert Length: 10000	Srd Error:	0.00			
	Plate: 0306	Row: J	Column: 08			
	Class: plasmid ends					
	High quality sequence stop: 98.					

ACCESSION A2566002
VERSION A2566002.1
KEYWORDS
SOURCE Plasmodium vivax (malaria parasite P. vivax)
ORGANISM Plasmodium vivax
REFERENCE
 1 (bases 1 to 981)
 Carlton, J.M.-R. and Dame, J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT
 Contact: Dame JB
 Dept. of Pathobiology, College of Veterinary Medicine
 University of Florida
 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
 Tel: 352 392 4700
 Fax: 352 392 9704
 Email: damej@email.vetmed.ufl.edu
 Seq primer: M13(-20) forward
Class: shotgun.
FEATURES
source
 1. .-98
 /organism="Plasmodium vivax"
 /mol_type="genomic DNA"
 /strain="Belam"
 /db_xref="taxon:5055"
 /dev_stage="asexual blood forms"
 /lab_host="Saimiri boliviensis"
 /clone_lab="Pv MBN #16 (amplified twice)"
 /note="Vector: Lambda ZAP II (Stratagene); individual clones excised into phagemid pBluescript; Site 1: EcoR I; Site 2: EcoR I; Genomic DNA was prepared from asynchronous blood stage forms of the Belam line of vivax grown in squirrel monkeys. Parasitized erythrocytes were purified

from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CFP1 cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclelease in the presence of 42.5% formamide at 50°C as described (Gajinski, K.D. et al. 1988; N.A.R. 15, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belém, Brazil 1980 by Mercia de Arnuda, adapted to Saimiri squirrel monkeys by Jung Gysin, and maintained since 1983 in

ORIGIN

Query Match Similarity 41.6%; Score 15.8; DB 8; Length 98;

Best Local Similarity 54.3%; Pred. No. 5.2e+04; Mismatches 4; Indels 0; Gaps 0;

Matches 19; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 CGUGCAUCUGAGAGCCGUNGGCGAAAUCA 36

Db 18 CTGCAAAGGGTATTCAGTAGGAGAAGGCA 52

RESULT 32

AT1702572

AT1702572

76 bp

mRNA

linear

EST

18-DSC-1999

DEFINITION

IMAGE:3477373 3', mRNA sequence.

ACCESSION

AT1702572

AT1702572.1

GI:4990472

VERSION

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens

REFERENCE

1 (bases 1 to 76)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LILN ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Inset Length: 564 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 65.

Location/Qualifiers

FEATURES

Source

1. .76

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="Taxon:9606"

/clone="IMSR:2347373"

/lab_host="BH10B"

/clone_lib="Soares_NFL_T_GBC_SI"

/note="Organ: pooled; Vector: pMT3D-Pac (Pharmacia) with

a modified polylinker; Site: 1; Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (Fetal lung NbH19W, testis NHT and B-cell in

NCI CGAP GC31) were mixed and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNA from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297880-302087, 682332-687239,

72908-728711, and 729096-73139. Subtraction by Bentu

Soares and M. Fatima Bonaldo.

"

FEATURES

Source

1. .41

/organism="Arabidopsis thaliana"

/mol_type="Genomic DNA"

/cultivar="Wasilewskia"

/db_xref="taxon:3702"

/clone="576H02"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

1. .41

/note="T-DNA flanking sequence

left border"

,

ORIGIN

Query Match Similarity 41.1%; Score 15.6; DB 1; Length 76;

Best Local Similarity 58.2%; Pred. No. 6.1e+04; Mismatches 4; Indels 0; Gaps 0;

Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAUAGAGGCCGUAGGCCGAAA 32

Db 13 GATGGCCCTTTAGCCGAAA 34

RESULT 33

W72704

W72704

76 bp

mRNA

linear

EST

17-OCT-1996

DEFINITION

2d71C05.81 Soares fetal_heart_NDH19W Homo sapiens cDNA clone IMAGE:346083, similar to PIR:A26882 A26882 pil2 hypothetical

ACCESSION

W72704

W72704.1

GI:1382701

SOURCE	Homo sapiens (human)	AUTHORS	Zambrowicz, B.P., Abuin,A., Ramirez-Solis,R., Edwards,J., Finch, R.A., Pigott,J., Beltranadelrio,H., Buxton,E.C., Edwards,J., Jaing,C., Fiddle, C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Jr., Kipp,P., Kohlhauf,B., Ma,Z.-O., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schirck,J., Shi,Z.-Z., Sparks,M.J., van Sligtenhoofst,I., Vogel,P., Walko,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
ORGANISM	Homo sapiens	REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo. (bases 1 to 76)
COMMENT	JOURNAL	AUTHORS	Hillier,L., Clark,N., Dubroque,T., Ellison,K., Hawkins,M., Holman,M., Hultman,M., Kubab,T., Le,M., Lennon,G., Marras,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
JOURNAL	The WashU-Merck EST Project	TITLE	The WashU-Merck EST Project
FEATURES	Unpublished (1995)	COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
Source		THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LINL ; CONTACT THE IMAGE CONSORTIUM (INFO@IMAGE.LINL.GOV) FOR FURTHER INFORMATION.	
		TRACE CONSIDERED OVERALL POOR QUALITY	
		Possible Reversed Clone: Similarity on wrong strand	
		Insert Length: 1248 Std Error: 0.00	
		Seq primer: mob REGA-ET	
FEATURES	High quality sequence stop: 1.	LOCATION/QUALIFIERS	
Source	1..76	/note="Organ: heart; Vector: pT7M3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCACCATGAGGGAGCGGCCATCTTTTTTTT 3']"; /clone="IMAGE:346088"; sex="unknown"; dev_stage="19 weeks"; /lab_host="DH110B (ampicillin resistant)"; /clone_1b="Soares fetal heart NBHH99W"	
ORIGIN		/note="Organ: heart; Vector: pT7M3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCACCATGAGGGAGCGGCCATCTTTTTTTT 3']"; /clone="IMAGE:346088"; sex="unknown"; dev_stage="19 weeks"; /lab_host="DH110B (ampicillin resistant)"; /clone_1b="Soares fetal heart NBHH99W"	
FEATURES	1..76	/organism="Homo sapiens"	
Source		/mol_type="mRNA"	
		/db_xref="GDB:1711463"	
		/db_xref="taxon:19606"	
		/clone="IMAGE:346088"	
		/sex="unknown"	
		/dev_stage="19 weeks"	
		/lab_host="DH110B (ampicillin resistant)"	
		/clone_1b="Soares fetal heart NBHH99W"	
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Contact: Rob Holt
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave., Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@ccgsc.ca
 Clones are derived from the bovine BAC library CHORI-240
 (<http://www.chori.org/bacpac/bovine240.html>). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 (<http://www.chori.org/bacpac/ordering-information.htm>). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.
 Plate: 311 row: L column: 11
 Seq primer: SP6
 Class: BAC ends.

FEATURES

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Location/Qualifiers
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 library (Male); produced by Pieter de Jong"
 library (Male); produced by Pieter de Jong"

ORIGIN

Query Match 40.5%; Score 15.4; DB 9; Length 51;
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 QY 5 CAUCUGAAGGCCGTTAGCCGA 29
 Db 26 CGACCTGTAGGGTCGTTGGCAA 50

Search completed: May 13, 2005, 17:51:09
 Job time : 1864.87 secs